us-10-017-410-1.rge

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AF282864 Mus muscu
BC059819 Mus muscu
BC050806084 Mouse DNA
BX324222 Mus muscu
AC120245 Rattus no
AC097362 Rattus no
AC097362 Rattus no
AC017081 Homo sapi
AC1206799 Sequence
AC17081 Sequence
G76816 S208P660FG
AX400443 Sequence
BV05534 S212P6219
CQ736906 Sequence
CQ74096 Sequence
AY071232 Drosophil
AR133976 Drosophil
AR133976 Cosophil
                                                                 .; Search time 16939.5 Seconds (without alignments) 11655.272 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                      Description
                                                                                                                                                                                                                      9053458
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                               4526729 seqs, 23644849745 residues
                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
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                                                                   November 20, 2004, 20:50:21
                                                                                                                                                                                                                                                                             Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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BV053534
CQ736905
CQ736906
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BX005084
BX324222
AC120245
AC097362
CQ842051
AK123581
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AK123581
                                              - nucleic search, using sw model
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AF323976
AK116177
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                                                                                                                                                              IDENTITY_NUC Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                              seq length: 0
seq length: 200000000
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Match Length DB
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gb htg: *
gb om: *
gb om: *
gb ow: *
gb ph: *
gb pl: *
gb ro: *
gb ro: *
gb v: *
gb v: *
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83.1 90370
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29.3 184163
17.3 2852
117.3 2852
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1222.4
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261.2
261.2
258
232.4
229.2
205
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510.8
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Perfect score:
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Maximum DB
                                              OM nucleic
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                                                                                                                                          Sequence:
                                                                                                                                                                                                 Searched:
                                                                     Run on:
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			!			KEYWORDS
	1683	1529	.1 GI:17529683	AF282864 AF282864.1	AF2 AF2	ACCESSION VERSION
mRNA, complete cds.	Mus musculus cancer related gene-liver 1	er	ulus canc	muscı		DEFINITION
linear ROD	4174 bp mRNA			AF282864	AF2	AF282864 LOCUS
						RESULT 1
	ALIGNMENTS					
AL670603 Mouse DNA	AL670603	10	7 173696	•	72	c 45
	AC108371	7		4		
	AC017406	~	m	1.9	77.8	0 4 1 8
	CC/31034	o u		-	4. P. L	
ACU93044 Drosophil	AC093044	m '	165585	CI.	95.6	
	AC009252	m		2	95.6	
	AE003665	m		2.2	92.6	
	AC004364	3		7	95.6	37
	AC017332	~	13715	2	92.6	
	C0605546	9			9 20	י ה
	CQ493050	o vo	2143	4 6	108	
CO492337 Sequence	CQ49259/	۰ م		9.0	108	c 32
	BD115297	9	358	2.7	114.2	31
	AX980438	9		2.7	114.2	30
	AR419744	9		2.7	14.2	50
	AC109451	~		3.0	124	28
	AL391834	, 0	-	1 6	124	
AK024898 Homo sabi	CQ605547	ه م	1917	w .	160.6	25
m	AF347023	10		4.2	173.8	
AF347024 Homo sapi	AF347024	σ		4.2	174.8	
	AX206797	9		4.2	174.8	22
	AC109451	~	219	4.4	183.6	
	AL158206	σ	163542	4.4	183.6	20 1

AF282864 4174 bp mRNA linear ROD 12-DEC-2001 Mus musculus cancer related gene-liver 1 mRNA, complete cds. AF282864 AF282864.1 GI:17529683	Mus musculus Mus musculus Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia: Eutheria: Rodenta, Sciuroquathi, Muridae, Murinae, Mus	e,T., Mador g and ident nomae 704-2712 (2	2 (bases I to 4174) Craveel, C.R. Jarkoe, T., Madore, S.J., Holt, A.L. and Farnham, P.J. Identification of genes deregulated in murine hepatocellular carcinomas using oligonucleotide microarrays and representational difference analysis Unpublished 3 (bases I to 4174) Farnham, P.J. and Graveel, C.R.	Submitted University 1	35862
RESULT 1 AF282864 LOCUS DEFINITION ACCESSION VERSION	KEYWOKDS SOURCE ORGANISM	REFERENCE AUTHORS TITLE JOURNAL MEDLINE PUBMED	REFERENCE AUTHORS TITLE JOURNAL REFERENCE AUTHORS TITLE	JOURNAL FEATURES SOURCE	CDS

us-10-017-410-1.rge

1021	TIGGAAGCTTTTGGTGTGTGTGTTGTTGTTGTTGTGTGTGTG
B 2 B 2 B 2 B 2 B 2 B 2 B 2 B 2 B 2 B 2	8 6 8 6 8 6 8 6 8 6
Query Matches	00

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LPPICMCLERQYATCENSGTYLIWTLLNVVGIGSVYFHATLSFLGQMLDELAILWYLM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GCTGCTCCGATGCTCCAGAGCGGCCATGGGCGCCCCGCACTGGTGGGACCACTGCGGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GTTCTACAACAGCATCAGCAACGTCTTGTTTTTACATTTACCTCCCATCTGCATGTGCTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          291 TGTAGTGGGGATTGGATCTGTTTCCATGCAACGCTGAGTTTTCCTGGGTCAGATGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TGATGAACTTGCCATTCTGTGGGTTCTGATGTGTGCTTTGGCCATGTGGGTTTCCCAGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TGATGAACTTGCCATTCTGTGGGTTCTGATGTGTGTGTTTGGCCATGTGGTTTTCCCAGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTATTTACCAAAGATCTTTCGGAATGACAGGGCAGGTTCAAGGCAGTGGTGTGTCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           430 GTCTGCAATTACAACGTGCTTGGCGTTTATCAAGCCCGCCATCAACAATATTTCCCTGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10 GCTGCTCCGATGCTCCAGAGCGGCCATGGGCGCCCCGCACTGGTGGGACCACCTGCGGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GTTCCGCCAGTACGCAACGTGCTTCAACAGCGGCATCTACTTAATATGGACGCTCCTAGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          550 GCGTGTGTTTTAAGCTGGGCCTCTTCTCTGGCCTCTGGTGGACTCTGGCTCTTCTTCTGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                453 GCGTGTGTTTAAGCTGGGCCTCTTCTCTGGCCTCTGGTGGACTCTGGTGGCTCTTTCTGCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      92.6%; Score 3864.4; 96.6%; Pred. No. 0;
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                                                                     'note="Vector: pYX-ASC"
                             host="DH10B
                                                                                                                                                                                                                                              gene="CRG-L1"
                                                                                                                                                                                                                                                                                      codon start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CAHKKSPVKIT
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                                                                                                                                                                                                                                                                                                                                                                                                    Straubberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Straubberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Altschul, S.E., Zeeberg, B., Buetc, Schemen, C.M., Schuler, G.D.,
Altschul, S.E., Jordan, H., Morce, T., Max, S.I., Wang, J., Hsieh, N.K.,
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Stapleron, M., Soares, M.M., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Uddin, T.B., Toshiyuki, S.
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Boask, S.A., McBwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
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Villalon, D.K., Wanny, D.M., Sodersen, E.D.,
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Garen, E.D.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Samailus, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
              Mus musculus cancer related gene-liver 1, mRNA (cDNA clone MGC:69583 IMAGE:6839525), complete cds.
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This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 21314857. Location/Qualifiers
1. 4078
/organism="Mus musculus"
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                                                                                                                                                                                                                                                                           Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Musina
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: nih.gov
Tissue procurement: Dr. James Lin, University of Iowa
CDNA Library Preparation: M. Bento Soares, University of Iowa
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
info@bcgsc.bc.ca
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/clone="MGC:69583 IMAGE:6839525"
/tissue_type="Brain"
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/strain="C57BL/6"
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During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission only a small overlap as described above.

Corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted; all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em: EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORNDED: Information the part of the clone and be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ROD 23-OCT-2003
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Bequence from clone RP24-468M3 on chromosome 4, complete
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 90370)
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Location/Qualifiers
                        4088 IGATAACCAIGGICAAIAITAAAGCCAAIAACIGGCAITITCIGIGAAIAAACAIGCAIA
                                                                                                    3993 IGATAACCATGGTCAATATTAAAGCCAATAACTGGCATTTTCTGTGAATAAACATGCATA
TIAACCATAGCTCTGGGAGGATTTACAGACCTTTTGCACTTTATGCTTTTTTGTGAACTC
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Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
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/db_xref="taxon:10090"
/chromosome="4"
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/clone lib="RPCI-24"
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1869 61968: gap of 100 bp
1869 83921: contig of 21953 bp in length
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3412 GAAGTGTTCCTTCTGTCTGCTTCCTTTGTAATGTGATCCACTCGGGGA 4991 GAAGTGTTCCTTCTTCTTCTCTTTTTTTTTTTTTTTTTT	DEFINITION Rattus norvegicus clone CH230-259012, WORKING DRAFT SEQUENCE, S and anordered pieces. ACCESSION AC120245 AC120245 AC120245 AC120245 AC120245 HTG: HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP. RETURN ACTORDER CONTROL (Norway rat) Rattus norvegicus (Norway rat) Rattus norveg
1932 TICKTROCARTITACCAACTCTCCCAGGTACCAACACACACTCATTGATTGCGATTTA 1391 19	3172 TCCAGAATCTTCTCCCTTCTGGTAGACATGACATGAGTGATGTCGTGACCACTGGG 3231 44751 TCCAGAATCTTCTCCCTTCTGGTAGACATCGATGAGTGATGTCGTGACCACTGGG 3231 44751 TCCAGAATCTTCTCCCTTTCTGGTAGACATCGATGAGTCATGTCGTGACCATGGG 44810 3232 CCCTGCATGGGTGTCGGGCTCTGTTCTGTCCGAATCTCAGGACACAGGG 3291 44811 CCCTGCATGGGTGTCGGGCTTCTGTTCCGGAATCTACCTGGACACAGGG 44870 3292 AAGCCATGAATGTTACCAAGTGGTCATGGCTGTCAGTGATTTTACAGTTTTGAACCATTA 3351 44871 AAGCCATGAATGTTACCAAGTGGTCATGGCTGTCAGTGATTTTACAGTTTTGAACCATTA 44930 3352 TTGGTTTTTAGGAGAATTCTTCTCTCTCTCTAGTGCCTGTGATGCCAAAGCCAACCCTTCA 44990 3352 TTGGTTTTTAGGAGAATTCTTCTCTCTCTAGTGCCTGTGATGCCAAAGCCAACCCTTCA 44990 44931 TTGGTTTTTAGGAGAATTCTTCTCTCTCTCTAGTGCCTTGATGCCAAAGCCAACCCTTCA 44990
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Submitted (15-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

Daylor Plaza, Houston, TX 77030, USA

On Nov 15, 2002 this sequence version replaced gi:22856351.

The sequence in this sequencing reads assembled using Atlas and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.ed/projects/rat/). Bach contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome
Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Clackrel, J., Clavez, D., Chen, G., Clackrel, R., Cave, M., Cree, A., D'Souza, L., Claveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L., Davila, M., L., Davila, R., Darang, C., Davy-Carroll, L., De Anda, C., Dederich, D., Delagado, O., Denson, S., Denamo, C., Ding, Y., Dinh, H., Duya, K., Bacchen, M., Eagan, M., Eagan, M., Eagan, M., Eagan, M., Eagan, M., Elas, T., Fan, G., Far, Fan, G., Fernandez, S., Finley, M., Flagg, N., Forbes, L., Foster, M., Foster, M., Ferser, C. M., Gabisi, A., Gatta, R., Garcia, A., Garner, M., Genera, M., Gunaratne, P., Haaland, W., Hamil, C., Hamilton, C., Hamilton, K., Harrandez, R., Hines, S., Hladun, S. L., Hodgson, A., Herrandez, R., Hines, S., Hladun, S. L., Hodgson, A., Herrandez, R., Hines, S., Hladun, S. L., Hodgson, A., Herrandez, R., Hines, S., Hladun, S. L., Hodgson, R., Johnson, R., Jackson, M., Lorenshwa, L., Loulseged, H., Lozdon, R., Martin, E., Mandum, A., Mandum, A., Mandum, A., Mandum, M., Mandum, M.,
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Submitted (05-MAY-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 184163)
Rat Genome Sequencing Consortium.
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ORIGIN
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                                                                                                                                Center: Baylor College of Medicine
Center code: BCM
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COMMENT

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Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
Contact: hgsc-help@bcm.tmc.edu
Center project Information
Center project name: GWTT
Center clone name: CH230-259012
Assembly program: Phrap; version 0.990329
Consensus quality: 176285 bases at least Q40
Consensus quality: 176285 bases at least Q30
Consensus quality: 177139 bases at least Q20
Consensus quality: 177139 bases at least Q20
Estimated insert size: 175972; sum-of-contigs estimation
Quality coverage: 7x in Q20 bases; sum-of-contigs estimation
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NOTE: This is a "working draft" sequence. It currently consists of 5 contigs. The true order of the pieces is not known and their order in this sequence record is
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          arbitrary, Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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/note="wgs_end_extension
clone_end:T7"
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clone_end:T7"
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/note="wgs_end_extension
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clone_end:T7"
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/db_xref="taxon:10116"
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40368. .40445
/note="clone_boundary
clone_end:T7
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171006. .172144
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complement(4969. .584;
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1723 CGTTTCTCTGCTGTTTTTAGGGATATGTGCTTCCTGAGTGACGTAGCCTCCCTAGGATG 1782 	1783 TGGGCCTCCGGCTTTTGTTTTCATAATACCTGGTGCTAACTGGTTTCTCAGAGCACTTTG 1842 	1843 CTCTTCTTGATGCTGGCGGTCACTACACTCTGATTGGCTGGC	1902 GAAGGGGAGACTCTGACATGAATGTCTCTCACCTGCATCCTACTGTCTTCACTGGGCTC 1961	1962 TCTTCAGGCTATGAAGTGGGTGTGGG-GTATCTCAGGGATGTTGTAACTCAGGCACCTT 2020 	2021 CTGCTTTCTGACATTCCATTGTCAGTGAGACTGCACTCGAGGACTCGAGTTGGAAC 2080	2081 ACCGTICTGAGTGTCCTGAGTCTGAAGGAGCTAGCTGCGGGTTCTGGCACTTCTAGG 2140	2141 ATCTCTTACTCTGTTTAGAACCTTCACAGGTACAAAGTGGGAACTGGACTTAAAGAGTT 2200	2201 TITAAAIGAAITAATICTOCITITGIGGCTIIGGAGITTIAAAAGIAACTIGCIG 2260 	2261 GGCTATTICTIGITTATAGTCACAAAIATTTATAGAACATGAAGGTGTAAAATAAGTTGT 2320 	2321 CTTTTATTAAATTCATAGCATTTACCAACTCCCCAGGTAGCAACACACAC	2377 TTGATTGGCGATTTACAAGGCAGGAATACTTGGTTTTGAATGATTGTATATGTCATTTA 2436 	2437 CTGTAGCTTAAAATATGTTTAAAATGACTTTGAGTGAAATGTTTGTGGGCAACCTAGGG 2494 	2495 GTTTATGGATCAGAATTGCGGCTGAGTCCTTTGGTTTTTGAGTCTAGAGTTTTCAGAGG 2554	2555 GCAAAATCAAACTAGCCTIGTITCTGGTTCATCTTACCAGGCTCGGGAGCTGCCCTTATA 2614	2615 TATTCTACATAAGGACTTATTATACATAAGTCTGTATAAATGTCCTGAAGATGACGCCTA 2674	2675 GCTGCCTTCATCTGGAAGGTCGTCTGGGGCTGGAAGTTGGTTCAACAGTTAA 2728 	2729 GAACCCGTGTTGCTCTCCCAGACGACCCAGCGACTTGTGAGGCTCAT 2777	AACCAGCAACTCCAGCCCTGGGGCATCTGACGCCCTCTTCTGACTTCTAAGG
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752 GAGCAAGGICCAGICAICAGAITCIGGCCGAGAAATGGGCTTTTATIGGIGTCCCT 811			TTTG 				GACC 		aacaaaaccaagtggggaaa 			GCAA 				CCTCGTTGTAATCGCGGAGGCACCTCTG-GAGGCTTGACTGTGGAGCGCCTGTGAAGATT		14020 TIGGAAAAGCITITCITAIIGGAAGCITACAGIGITGITGCTCCAAGACICTGACCC 14079

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Submitted (19-MXY-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA ON May 9, 2003 this sequence version replaced gi:24956965.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas and whole genome shotgun sequencing reads assembled using Atlas in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome table.
                                                                                                                                                                                                       Direct Submission
Submitted (17-OCT-2001) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html)
NOTE: This sequence may represent more than one clone.
NOTE: This is a 'working draft' sequence. It currently consists of 2 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Assembly program: Allas, Consensus quality: 241576 bases at least Q40 Consensus quality: 241576 bases at least Q30 Consensus quality: 245010 bases at least Q30 Estimated insert size: 253391; sum-of-contigs estimation Quality coverage: 7x in Q20 bases; sum-of-contigs estimation
       Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   203; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2; Length 249734;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Center: Baylor College of Medicine Center code: BCM
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Center project name: GAHA
Center clone name: CH230-3E15
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                                                                                                                                                                                                                                                                                                                                                         3 (bases 1 to 249734)
Rat Genome Sequencing Consortium.
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/db_xref="taxon:10116"
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                                    Weinstock, G. and Gibbs, R.A.
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Worley, K.C.
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15178 CATGCATGTGGTACACCTATGCATACAGGCAAGCCAAGTCATTCGTACATGTAAAGT---- 15233
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae;
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HTG: HTGS PHASE1; HTGS DRAFT; HTGS_FULLTOP.
Rattus norvegicus (Norway rat)
Rattus norvegicus
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Sugiyama,T., Irie,R., Otsuki,T., Sato,H., Wakamateu,A., Ishii,S.,
Yamamoto,J., Isono,Y., Kawai-Hio,Y., Saito,K., Nishikawa,T.,
Kimura,K., Yamashita,H., Mateuo,K., Nakamura,Y., Sekine,M.,
Kikuchi,H., Kanda,K., Wagatsuma,M., Murakawa,K., Kanehori,K.,
Takahashi-Yahii,A., Oshima,A., Sugiyama,A., Kawakami,B., Suzuki,Y.,
Sugano,S., Nagahari,K., Masuho,Y., Nagai,K. and Isogai,T.
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Isogai, T. and Yamamoto, J.

Direct Submission

Submitted (15-Jun-2003) Takao Isogai, FLJ Project (HRI Team); 2-6-7

Kazusa-Kamatari, Kisarazu, Chiba 292-0818, Japan

(E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)

NEDO human CDNA sequencing project supported by Ministry of

Beconomy, Trade and Industry of Japan; CDNA full insert sequencing:

Research Association for Biotechnology (RAB); CDNA library
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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494 GTATCTACCAAAGATCTTTCGGAATGACCGGGGTAGGTTCAAGGTGGTGGTCAGTGTCCT
                                                     GTCTGCAATTACAACGTGCTTGGCGTTTATCAAGCCCGCCATCAACAATATTTCCCTGAT
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        GCTGCCTTTGTCTGAAAGGGCCCCGAGCTGTCTGGGGCTGGAGCTGGTTCAGCCGATAA 151052
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Full-length human cdna
Patent: EP 1440991-A 698 28-JUL-2004;
Research Association for Biotechnology (JP)
Location/Qualifiers
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                 GAACCCGTGTTGCTCTCCCAG-------ACGACCCAGCGACTTGTGAGGCTCAT
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0; Mismatches 143;
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/mol type="unassigned DNA"
/db_xref="taxon:9606"
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Sequence 698 from Patent BP1440981.
CQ842051
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Web site: http://genome.wustl.edu/gsc
Contact: sapiens@watson.wustl.edu
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construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: HRI and RAB, annotation: HRI and RAB.
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/ organism="Homo sapiens"

/organism="Homo sapiens"

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/db_xref="crowd.sell"

/clone="crowd.sell"

/lissue="crowd.sell"

/lone lib="crowd.sell"

/note="cloning vector: pME185FL3"
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PRI 09-JAN-2002 1030 AGTGGGCTTCCTTTGCTAGGAAGACAGCCAAGGAAGTTCGAATAGTTGGGGGTGTGGGCTA 1089 Direct Submission Submitted (09-DBC-1999) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, USA Aresecerrearresrerecerarererecerecererereceaecaacaareareaer 973 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo. 1 (Bases 1 to 14942) Sulston,J.E. and Waterston,R. Direct Submission Submitted (09-JAN-2002) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, On Jan 9, 2002 this sequence version replaced gi:14165368. 910 GCTGGGCTTCGTTTGCTAGCAAAGATGGCTGAGGGGGTTGAGGAATTGGTGTGGTGTGGG CAAGATCACGTGATGGCAAGGCAGTGACCAGCTTCTACTTCTATTCGAGTGCGC AC017081 149462 bp DNA linear PRI 09-JA Homo sapiens BAC clone RP11-470J24 from 2, complete seguence. AC017081 Center: Washington University Genome Sequencing Center 2 (bases 1 to 149462)
Mguyen,C., Doebber,A. and Kozlowicz,A.
The sequence of Homo sapiens BAC clone RP11-470J24
Unpublished (2001)

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by This sequence was finished as follows unless otherwise noted:

ď. MAPPING INFORMATION: Mapping information for this clone was provided by Dr. John

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21685. .21819
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22160. .22840
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22878. .23228
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8000. 8436
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3. .21566
family="AT_rich"
'rpt_family="AT_rich"
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0320. .1034
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12592. 12706
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12707. 12952
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13139, 16061
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/rpt_family="L2"
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0280. .10305
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family="L1"
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33787 .9422
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                                                                                The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at the Roswell Park Cancer Institute (http://bacpac.med.buffalo.edu)
     McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see http://genome.wustl.edu/gsc
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965. - 1037
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1127. :1561
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                                                                                                                                                                                                                                                    The clone sequenced to the left is RP11-310K15, 2000 bp overlap: the clone sequenced to the right is RP11-156A1, 2000 bp overlap. Actual start of this clone is at base position 190775 of RP11-310K15; actual end is at base position 28935 of RP11-156A1.
                                                                                                                                                                                                                                                                                                                                  The sequence between 81601 and 81703 is covered only by a pcr product of clone DNA. Unresolved tandem repeat regions exist between 81548 and 83183, 126196 and 127426.

Location/Qualifiers
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| Chromosome="2"
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NEIGHBORING SEQUENCE INFORMATION:
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.17835

17161

.21684

RESULT 10 AZ206799 LOCUS DEFINITION Sequence 6 from Patent W00155408. ACCESSION AZ206799 VERSION AZ206799 VERSION AZ206799 VERSION AZ206799. GETWORDS CONGANISM Homo sapiens (human) ORGANISM Homo sapiens (human) Rukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;	Primates; Catarrhini; Hominidae; it,M. 6 02-AUG-2001;	Memorec Medical Molecular Research Cologne Stoffel GmbH (DE) FEATURES Location/Qualifiers 1812 1822 /organism="Homo sapiens" /mol_type="unassigned DNA"	ORIGIN Query Match Best Local Similarity 87.9%; Pred. No. 1.38-165; Matches 725; Conservative 0; Mismatches 97; Indels 3; Gaps 1;	CCGCACTGGTGGCACCTGCGGCTGGCAGTTCGGAGTTGGTGC 94	OY 95 GAGGACAACTATCGTGCCTGCCATTGCCGAGTTCTACAACACGATCAGCAACGT 154	OY 155 TIGITITICALITIACCICCCAICTGCAIGIGCTIGITICCGCCAGIACGCAACGIGCTIC 214	OY 215 AACAGGGGATCTACTTAATATGAGGGCTCCTAGTTGTAGTGGGGATTGGATCTGTCTAC 274	Oy 275 TTCCATGCAACGCTGAGTTTCCTGGGTCAGATGCTTGATGAACTTCTGTGGGTT 334	Qy 335 CTGARGTGTGCCATGTGGTTTCCCAGGAGGTATTACCAAAGATCTTTCGGAAT 394 Db 298 CTGARGTGTGCTTCGGTCATGTGGTTCCCCAGAAGGTATCTACCAAAGATCTTTCGGAAT 357	Qy 395 GACAGGGCAGGTTCAAGGCAGTGGTGTCTCCTGCTGCCAATTACAACGTGCTTGGCG 454	OY 455 TTTATCAAGCCGGCATCAACAATATTTCCCTGATGATTCTGGGACTTCCATGCACTGCG 514 Db	OY 515 CTGCTTGTTGCAGAGCTGAAGAGGTGTGACAATGTGCGTGTTTAAGCTGGGCCTCTTC 574	Qy 575 TCTGGCCTCTGGTGGCTCTTCTGCTGGTTGAGCGACCAAGCCTTCTGTGAG 634	Ay 635 CTGCTCCTCCTCCTTCCCTACCTGCACTGTGTGGCATATTCTCATCTGCCTT 694	Qy 695 GCTTCGTACCTGGGCTGTGTGTCTTCGCCTACTTTGATGCTGCCTCAGAGATACCTGAG 754
Query Match 16.9%; Score 705; DB 9; Length 149462; Best Local Similarity 84.4%; Pred. No. 2.7e-179; Indels 6; Gaps Matches 818; Conservative 0; Mismatches 145; Indels 6; Gaps 10 GCTGCTCCCGATGCTCCAGAGGGCCCCACCCCCACTGGTGGACCACTGGTGGGACCAGCTGCTGGAGGCCCCCCACTGGTGGACTGCTGCTGCTGCTGCAGGCCCTGCAGGCCCCCCACTGGTGGAACTGCTGCTGCTGCTGCAGGCCAGCTGCAGGCCAGCTGCTGCAGGCCAGCTGCCAGCTGCCAGCTGCCAGCTGCCAGCTGCCATGCTGCCAGCTGCCATGCTGCCATGCTGCTGATGCCCATGCTGCTGCTGTGCCATGCTGCTGATGCCCAGGTGCCATGCTGCTGATGCCCATGCTGCTGATGCCCAGTGCAGTGCCAGTGCAGTGCAGTGCCAGTGCAGG	Db 136886 TGGCAGCTCGGAGGTGGACTGGCGCGAGGACAACTACACCATCGTGCCTGCTGCCGGA 136827	190 GTTCCGCCAGTACGCAACGTGCTTCAACAGCGGCATCTACTTAATATGGACGCTCCTAGT	250 IGHACIGGGANICGGANICGGANGGANGGANGGANGGANGGANGGANGGANGGANGGA	DD 138848 TGAACTIGCAGICCTITGGGTTCTGGTGTCTTCGGTTCCCCAGAG 136589 QY 370 GTATTTACCAAAGATCTTTCGGAATGACAGGCAGGTTCAAGGCAGTGGTGTGTGT	CTGAT 489 CTGAT 13646	AATGT AACAT	Qy 550 GCGTGTGTTTAAGCTGGCCTCTTCTCTGGTGACTCTGGCTGCTCTTCTGCTG 609 Db 136408 GCGTGTGTTTAAGCTGGGCCTCTTCTCGGGCCTCTGGTGGACCCTGGCCCTGGCCCTGGCCTTTTTAGCTG 136349		Qy 670 IGIGIGGCATATICICATCTGCTTGGTACCTGGGCTGTGTGCTTCGCCTACCT 729		Qy 790 AIGGGCTTTTATTGGTGCCTTATGTGTCCCTTCTGTGGCCACAAGAAGTCGCCAGT 849 Db 136168 AIGGGCCTTCATTGGTGCCCTATGTGTCCCTCCTGTGTGCCAAAAAAAA	909	910 GCTGGGCTTCGTTTGCTAGCAAAGATGGCTGAGGGGTTGAGGAATTGGTGTGGTGGGGGTTGAGGAATTGGTGTGGTG	970 IGTITAAA 978	

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3792 CCAACAACACATCTTTGGCCAGATTGGGATTCTCAATAGATTTTATAGACATTATTCTCC 3851
                  TITAAAATICIGCICCITIGIGAICIAACIGGACCACIGIGCCIGACCICCCIAGGIIAA
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Sequence 119 from Patent WO0210453.
AX400443.1 GI:21336623
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                                                                                                                                                                                                                                                                                                                             Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  as STSs and 81,000 SNPs were annotated with alleles from C57BL/6J and the Strain from which the particular read came. The validation rate for these SNPs was estimated at approximately 98%.
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                                                       GGGCTTTTATTGGTCCCTTATGTGTCCCTTCTGTGTGCCCCACAAGAAGTCGCCAGTCA
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                                    CAAGGICCAGICATCAGATICIGGCCCAGCGAGAAAIGGGCTITITATIGGIGICCCTITAI
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                                                                                                      815 GIGICCCTICIGIGICCCACAAGAAGICGCCAGICAAGAICACG 859
                                                                                                                          778 GTGTCCCTCTGTGTGCCAACAAGAAATCATCAGTCAAGACCACG 822
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/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="12951/SvImJ"
/db_xref="taxon:10090"
/map="+ 4 20-461 84241674-84242112"
/clone lib="12951/SvImJ"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         320 Charles Street, Cambridge, MA 02141, USA
Tel: 6172521477
Fax: 6172580903
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 510.8; DB 1;
Pred. No. 8.4e-127;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Polymorphism Structure in the Mouse Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: kersli@genome.wi.mit.edu
Primer A: None
Primer B: None
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Kerstin Lindblad-Toh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 99.1%;
Matches 525; Conservative 0
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1031
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
                         421 CCTGATAAACAAGACCTTCTGATTTGGTGATGAAAGGTTCCAGAACTTTTCATTTTGCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3557 ATTCTATTGGTTGGATTTCTCAGGAGTCTGAATCTTCCCTCACGAGTCCTCTCTCCCAA
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                                                                                                                                                                                                              1092 CTGGGTTATGTCCATAATGACATCAACAGAGTAGTTCTTTGGGAGACCTAGGGCAACCCA
                                                                                                                                                                                                                                                                       301 crederrargrecarandacaccaacadagracrerraggagaccraggecaacca
                                                                                                                                                                                                                                                                                                                                                                                                                                        1209 CCTGATAAACAAGACCTTCTGATTTGGTGATGAAAGGTTCCAGAACTTTTCATTTTGCCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1269 GGAGAAACTGTCCTTCAACAAACCAAGTGGGCAAAACACGTGTGGGGGG 1318
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Molecular toxicology modeling
Patent: WO 0210453-A 119 07-FEB-2002;
Gene Logic, Inc. (US)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
9.6%; Score 400.4; DB 6; Length 595;
Best Local Similarity 87.9%; Pred. No. 7.8e-97;
Matches 531; Conservative 0; Mismatches 56; Indels 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  481 GGAGAAACTGTCCTTCAACAAAACCAAGTGGGCAAAAACAGGGGGGG
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/organism="Rattus norvegicus"
/mol_type="unassigned DNA"
/hob_tref="texon:10116"
/note="EMBL/GenBank Accession No. AA848826"
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Kits, such as nucleic acid arrays, comprising a majority of
humanexons or transcripts, for detecting expression and other uses
                                                                                                                                                                                                                                                                                                                             724 AIAIATTTATAGACATTATTTCCCCCCCACAGACTTTAAAACATGGCTTGTGTCTTTCCTTA
                                                                                                                                                                                                                                                                                                                                                                                                                  664 CACATCCGGTCAGATTTAAAACTATTTTATAACCACAGGAATTAAAACCAAGGAAATAGAG
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                                                                                                                                                                                                                                                         784 ACCTGGGTGCTGTTGGTCCCACTGGCCAACAACACATCTTTGGCCAGATTGGGATTCTCA
                                                                                                                                                                                                                                                                                                     3827 ATAGATITITATAGACATTATTCTCCCACAGACTTTAAAACATGGCTTGTGTTTTCCATA
                                                                                                                                                                                                                                                                                                                                                                                           3887 CACATCCGGTCAGATTTAAAACTATTTATAACCACAGGAATTAAACCAAGCAAATAGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 604 TACTITCAGATATACACTGTGTTTCATACTTTATGTAGAGTGTGCTATGTATATGTAGGCGGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        484 TITAIGCITITITGIGAACICIGAIAACCAIGGICAATAITAAAGCCATTAACIGGCATT
                                                                                                                                                                                                              3767 ACCTGGGTGCTGTTGGTCCCACTGGCCAACACACATCTTTGGCCAGATTGGGATTCTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                544 TGTACCCTGGCTGAAGTAATATTAACCATAGCTCTGGGAAGGATTACAGACCTTTTGCAC
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Eutele
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                      0;
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                                                                                                                                                                      4; Indels
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      /map="- 4 22-692 84245395-84244718"
/clone lib="CZECHII/Bi"
<1. .>784
                                                                                                                            DB 11;
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                                                                                                                                                 .4e-92;
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Patent: WO 02068579-A 22839 06-SEP-2002;
PE Corporation (NY) (US)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6.3%; Score 261.2; DB 6
89.5%; Pred. No. 4.5e-59;
iive 0; Mismatches 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CQ736905 315 bp DNA Sequence 22839 from Patent WO02068579. CQ736905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TTCTGTGAATAACATGCATATGTATCTA 4155
                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           424 TTCTGTGAATAAACATGCATATGTATCTA 396
                                                                                                                          Score 382.6;
Pred. No. 5.4
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Location/Qualifiers
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                                                                                                                      9.2%;
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                                                                                                                                               Similarity
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Best Local Similarity
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Matches 385; C
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Wade, C.M., Kulbokas, E.J. III, Kirby, A.W., Zody, M.C., Mullikin, J.C., Lander, E.S., Lindblad-Toh, K. and Daly, M.J.
The mosaic structure of variation in the laboratory mouse genome Nature 420 (6915), 574-578 (2002)
                                                                                                                                                             3910 ATTITIATAACCACAGGAATTAAACCAAGCAAATAGAGTACTTTCAGATATAAACTGTGTT 3969
                                                                                                                                                                                                                                                   3970 TCATACTTTATGTAGAGTGTGCTATGTATAGGCGGTATGTACCCTGGCTGAAGTAATATT 4029
                                                                                                                                                                                                                                                                                                                                               4088
                                                                                                                                                                                                                                                                                                                                                                                                                                1089 GATAACCAIGGICAATATTAAAGCCAATAACIGGCATTTTCTGIGAATAAACAIGCATAT 4148
                                                                       CACAGACTTT - - AAAACATGGCTTGTGTCTTTCCATACACGGTCGGTCAGATTTAAAACT 3909
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   as STSs and 81,000 SNPs were annotated with alleles from C57BL/6J and the strain from which the particular read came. The validation rate for these SNPs was estimated at approximately 98%. Location/Qualifiers
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298 CACAGACTITAAAAAACAIGGCGIGIGICITITICCIACACA---AGICAGAITIAAAACI
                                                                                                                                                                                             241 ATTITATAACTACAATAATTCAACCAAGCAAATAGAGTATTTTCAGATATATGC--CATT
                                                                                                                                                                                                                                                                                               183 TTATACTTTATGTAGAGTGTGCTATGTACAGGTGGCATGTACCCTGGCTGAGGTAACATT
                                                                                                                                                                                                                                                                                                                                                                    123 AGTCATTGCTCTGGG-GGATTTACAGATCTTTTGCACTTTTTGTGAACTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                       64 GATAACCATCACATAAAGCCATTAACAGGCATTTCTGTGAATAAACATTTATGT
                                                                                                                                                                                                                                                                                                                                          4030 AACCATAGCTCTGGGAGGATTTACAGACCTTTTGCACTTTATGC-TTTTTTGTGAACTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Kerstin Lindblad-Toh
Whitehead Institute for Biomedical Research, Center for Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BV053534 11near STS 31-MAS S212P6219FA6.T0 CZECHII/Ei Mus musculus STS genomic, sequence
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/organism="Mus musculus"
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Tel: 6172521477
Fax: 6172580903
Email: kersli@genome.wi.mit.edu
Primer A: None
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/strain="CZECHII/Ei"
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RESULT 13 BV053534/c

DEFINITION

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS

TITLE JOURNAL MEDLINE PUBMED COMMENT

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Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W.
Kits, such as nucleic acid arrays, comprising a majority of humanexons or transcripts, for detecting expression and other uses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         668
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62 GGATCAGTGACCGAGCTTTCTGCGAGCTGCTGTCATCCTTCAACTTCCCCTACCTGCACT 121
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                                                                                                                                                                                                                                                                                                                               Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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PE Corporation (NY) (US)
Location/Qualifiers
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Sequence 22840 from Patent WO02068579.
CQ736906.1 GI:42333767
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Matches 281; Conservative
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Abv28857 Human pro
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Continuation (4 of
Ada11938 Rice gene
Adc87616 Human GPC
Adc87192 Mouse USH
Ada71938 Rice gene
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Ada62903 Mouse Mcm
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product= "Liver tumour marker protein, CRG-L1"
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                 ABV23021
ABX16390_3
ADA71938
                                                           ADC87616
ADM80713
ABK47192
ADA71938
ABL32061
ADA02933
ADM0285473
ADM92873
ADM02795
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ADA02903
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ADL95495
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ABS56565
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P-PSDB; ABG32880.
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   US2002115094-A1.
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Acc56961 Human bla
Adn38833 Cancer/an
Ads54149 Human cer
Ad121948 Novel hum
Abk6212 Rat seque
Ad16640 Human 3T3
Ad106640 Human 3T3
Ad106642 Human 3T3
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Ad1566 Human Dol
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                    GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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     AGGGCAACCCAAAGTTTCTTGCTGGAGAGGGTAGCTTGCTGTTTCCACTTTCCAGACT
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in normal liver tissues, designated CRG-Li. Also included are the encoding polymuclectides (in the case of the human sequence, mapping to chromosome 9p), expression constructs, host cells, anti-CRG-Li antibodies, identifying modulators of CRG-Li, and the use of the CRG-Li sequence in the diagnosis of hepatocellular cancer in tumour cells from liver of a human or non-human animal. The CRG-Li protein and polymucleotide are useful as diagnostic markers for a liver cancer in humans and non-human animals, and as a system for assessing putative therapeutic agents. The present sequence encodes mouse CRG-Li
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Detecting a bladder cancer-associated transcript in a cell from a patient, comprises contacting a biological sample from the patient with a bladder cancer-associated polynucleotide or antibody.
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03-AUG-2001, 2001US-0310099P.
08-NOV-2001, 2001US-0343705P.
13-NOV-2001, 2001US-0350666P.
12-APR-2002, 2002US-0372246P.
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Matches 823; Conservative
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GTCTGCAATTACAACGTGCTTGGCGTTTATCAAGCCCGCCATCAACAATATTTCCCTGAT

GTATTTACCAAAGATCTTTCGGAAATGACAGGGCAGGTTCAAGGCAGTGGTGTGTCTT

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602 GCGTGTGTTTAAGCTGGGCCTCTTCTCGGGCCTCTGGTGGACCCTGGCCCTGTTCTGCTG GATCAGCGACCAAGCCTTCTGTGAGCTGCTCTCCTCTTTCACTTCCCCTACCTGCACTG GATCAGTGACCGAGCTTTCTGCGAGCTGCTGTCATCCTTCAACTTCCCTACCTGCACTG

CATGTGGCACATCCTCATCTGCCTTGCTGCCTACCTGGGCTGTGTATGCTTTGCCTACTT

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Determining the presence or absence of a pathological cell in a patient, useful for diagnosing, prognosing or treating cancer, comprises detecting a nucleic acid in a biological sample. fibrotic disorder; psoriasis; ischaemia; heart disease; atherosclerosis; inflammatory disease; autoimmune disease; retinal neovascularistation syndrome; scarring; uterine fibroid; detection; diagnosis; prognosis; drug screening; drug targeting; wound healing; contraception; cytostatic; cardiant; immunomodulatory; vulnerary; gene therapy; vaccine; gene; ss. Gish KC, Glynne R, Hevezi PA; Wilson KE, Zlotnik A; Sequence 4212 BP; 1047 A; 894 C; 932 G; 1339 T; 0 U; 0 Other; sequence represents a nucleic acid sequence of the invention. Claim 8; SEQ ID NO 151; 1385pp; English. Aziz N, Ginsburg WM, Murray R, Watson SR, 2001US-03324(4F) 2001US-0334393P 2001US-0334393P 2001US-034721IP 2002US-034721IP 2002US-035250P 2002US-035514P 2002US-035514P (EOSB-) EOS BIOTECHNOLOGY INC 2002US-0396839P. 2002US-0397775P. 2002US-0397845P. 2002WO-US036810 2002US-0370110P. 2002US-0372246P. 2002US-0386614P. 2002US-0409450P 2003-468649/44. Aziz N, P-PSDB; ADN38834. 29-MAR-2002; 04-APR-2002; 12-APR-2002; 13-NOV-2002; Homo sapiens 03-DEC-2001; 14-DEC-2001; 08-JAN-2002; 10-JAN-2002; 05-JUN-2002; 08-FEB-2002; 13-FEB-2002; 20-FEB-2002;

The invention relates to nucleic acids and proteins (ADN38683-ADN40064)
whose expression is upregulated or downregulated in specific cancers or
other diseases such as andjogenic or fibratic disorders, and to methods
of determining the presence or absence of a pathological cell in a

patient by detecting a nucleic acid at least 80% identical to those of
the invention or by detecting a polypeptide of the invention. The
invention also relates to expression vectors and host cells comprising a

nucleic acid of the invention; antibodies which specifically bind a

polypeptide of the invention; use of such antibodies for drug targeting;
and methods of screening for modulators of activity or expression of the
polypeptides and nucleic acids. The nucleic acids, polypeptides,
antibodies and methods are useful for diagnosing, prognosing and treating
cancer and other conditions such as psortasis, ischaemia, heart disease,
also be useful in wound healing and un cerine fibroids. They may
also be useful in wound healing and in contraception.

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standard; cDNA; 828 BP.
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Query Match 17.3%; Score 723.8; DB 11; Length Best Local Similarity 84.9%; Pred. No. 5.5e-189; Matches 823; Conservative 0; Mismatches 142; Indels

958 AGTGGGCTTCCTTTGCTAGGAAGACAGCCAAGGGAGTTCGAATAGTTGGGCTATGTG

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GCTGGGCTTCGTTTGCTAGCAAAGATGGCTGAGGGGGTTGAGGAATTGGTGTGGTGTGGG 969

TGATGCTGCCTCAGAGATACCTGAGCTCCAGTCATCAGATTCTGGCCCCAGCGAGAA

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GACAGGGTAGGTTCAAGGTGGTGGTCAGTGTCTGTCTGCGGTTACGACGTGCCTGGCA 420
241 TTCCATTITACCCTTAGTTTCTTGGGTCAGATGCTTGATGAACTTGCAGTCCTTTGGGTT 300
                                                            GACAGGGCAGGTTCAAGGCAGTGTGTGTGTCTGCAATTACAACGTGCTTGGCG 454
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09-MAR-2000; 2000DE-01011392.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GAGGACAACTACACTATCGTGCCTGCCATTGCCGAGTTCTACAACACGGATCAGCAACGTC 154
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to a polypeptide designated as CRG-LII), which is differentially expressed in liver tumours relative to normal expression in normal liver tissues, designated CRG-LII. Also included are the encoding polymucleotides (in the case of the human sequence, mapping to chromosome 9p), expression constructs, host cells, anti-CRG-LI antibodies, identifying modulators of CRG-LII, and the use of the CRG-LII sequence in the diagnosts of hepatocellular cancer in tumour cells from polymucleotide are useful as diagnostic markers for a liver cancer in humans and non-human animal: The CRG-LII protein and humans and non-human animals, and as a system for assessing putative therapeutic agents. The present sequence encodes human CRG-LI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel polypeptide designated as CRG-L1, useful as diagnostic marker for liver cancer, is differentially expressed in liver tumors relative to normal liver tissues.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AACAGGGGCATCTAATAATAAGACGCTCCTAGTTGTAGTGGGGATTGGATCTGTCTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TTCCATGCAACGCTGAGTTTCCTGGGTCAGATGCTTGATGAACTTGCCGTTCTGTGGGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          THGITTITCATTITACCICCCATCIGCATGIGCTIGITCCGCCAGTACGCAACGIGCTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 ATGGGCGCCCCGCACTGGTGGAGCCAGCTGCAGGCTGGTAGCTCGGAGGTGGACTGGTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATGGGCGCCCCCCACTGGTGGGACCACTGCGGGCTGGCAGTTCGGAGGTGGATTGGTGC
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                                                                                                                                                                                             Location/Qualifiers
1. .828
|*tags a
|product= "Liver tumour marker protein, CRG-L1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 664.8; DB 6; Length 828;
Pred. No. 4.7e-173;
0; Mismatches 102; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 828 BP; 157 A; 216 C; 211 G; 244 T; 0 U; 0 Other;
                                                                     Human cDNA encoding a liver tumour marker protein, CRG-L1.
                                                                                                   Human; ss; gene; liver cancer; liver tumour; CRG-L1; hepatocellular cancer; chromosome 9p.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 2; Page 8; 11pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 15.9%;
Best Local Similarity 87.7%;
Matches 726; Conservative
                                                                                                                                                                                                                                                                                                                                                             14-DEC-2001; 2001US-00017410
                                                                                                                                                                                                                                                                                                                                                                                               14-DEC-2000; 2000US-0255674P
                                   (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                  (FARN/) FARNHAM P J. (GRAV/) GRAVEEL C R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2002-706409/76.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P-PSDB; ABG32881
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                                                                                                                                                               Homo sapiens
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This invention describes novel human ceramidase (I) containing a specific structural motif which has antiproliferative, anticancer, anti-eczema, antipsoriasis and dermatological activity. (I) cleave ceramide, resulting in formation of sphingosine. (I) or the nucleic acid (II) encoding it, are used for diagnosis, prevention or treatment of diseases associated with ceramide defects, particularly altered cell proliferation (cancer) por altered ceramide layers on the skin (neurodermatitis, eczema, psoriasis), also for targeted modification of the permeability barrier by ceramidase or its activators, e.g. for transcutaneous delivery of substances. Specifically they are used for diagnosis of ichthyosis, particularly lamellar ichthyosis ICR2. (I) can also be used in cosmetics. This sequence encodes human ceramidase X3
                                                                                                              New ceramidase containing specific structural motif, useful for diagnosis, prevention and treatment of ceramidase defects, e.g. ichthyosis, also in cosmetics.
                                                                                                                                                                                                          Claim 3; Page 17; 31pp; German.
  Conradt M;
                                             2001-483256/52.
                                                                     P-PSDB; AAB86365
  Hofmann K,
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Sequence 822 BP; 153 A; 225 C; 209 G; 235 T; 0 U; 0 Other;

154 120 214 180 274 237 514 ITCCATGCAACGCTGAGTTTCCTGGGTCAGATGCTTGATGAACTTGCCATTCTGTGGGTT 334 297 CTGAIGTGTGTGTTTGGCCAIGTGGTTTTCCCAGGAGGTATTTACCAAAGATCTTTCGGAAT 394 GACAGGGCAGGTTCAAGGCAGTGGTGTGTCTGTGTGTGCAATTACAACGTGCTTGGCG 454 daccaddaraddricaaddrocridricricridrorgcadriangacdridcorddca 417 irigicia a general canta de la contra del la contra del la contra del la contra del la contra de la contra de la contra del la contra de la contra del la contra 574 537 634 597 94 9 694 657 61 GAGGACAACTACACCATCGTGCCTGTCGCCGAGTTCTATAACATGATCAGCAATGTC 121 Tratriticarritacceccarciecarerecterrighticercaeranecarectre 215 AACAGCGGCATCTACTTAATATGGACGCTCCTAGTTGTAGTGGGGGATTGGATCTGTCTAC ATGGGCGCCCCGCACTGGTGGGACCACCTGCGGGCTGGCAGTTCGGAGGTGGATTGGTGC GAGGACAACTACACTATGGTGCCTGCCATTGCCGAGTTCTACAACACGATCAGCAACGTC TIGITITICATITIACCICCCATCIGCAIGIGCIIGITICCGCCAGAACGAACGIGCTIC TTTATCAAGCCCGCCATCAACAATATTTCCCTGATGATTCTGGGACTTCCATGCACTGCG Gaps CTGCTTGTTGCAGAGCTGAGAGGTGTGACAATGTGCGTGTGTTTAAGCTGGGCTCTTT TCTGGCCTCTGGTGGACTCTGTTCTGCTGGATCAGCGACCAAGCCTTCTGTGAG CIGCICTCCTCTTTCACTTCCCCTACCTGCACTGTGTGGCATATTCTCATCTGCCTT 3; 97; Indels Score 653.8; DB 4; Pred. No. 5.3e-170; 0; Mismatches 15.7%; Query Match Best Local Similarity 87.9° Matches 725; Conservative 35 Н 95 155 181 275 238 335 298 395 358 418 515 478 575 455 염 ઠે ò g ò g 셤 à à g à qq ⋩ d à 쉱 à d ₽ g

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The invention relates to an isolated polymucleotide encoding a polypeptide with biological activity. The polymucleotides and polypeptides are useful in diagnostics, forenaics, gene mapping, identification of mutations responsible for genetic disorders and other traits, to assess biodiversity, as nutritional sources or supplements. The polymucleotides may also be used as molecular weight markers, chromosome markers or map related gene positions, or as an antigen to raise anti-DNA antibodies or elicit immune response. The polypeptides are useful for raising antibodies, as markers for tissues in which the corresponding polypeptide is expressed, for re-engineering damaged or diseased tissues, for treating myeloid or lymphoid cell disorders, in corresponding to the corresponding myeloid or lymphoid cell disorders, in regeneration, in wound healing, in tissue growth or regeneration, in wound healing, in tissue repair and replacement, in healing of burns, incisions and ulcers, and in treating cancer. The present sequence represents cDNA encoding a novel human protein.
                                                                                717
                                                                                                                                                   814
   GCTTCGTACCTGGGCTGTGTGTGCTTCGCCTACTTTGATGCTGCCTCAGAGATACCTGAG 754
                                                                                                                                                                                                                  777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       forensic; nutritional source; damaged tissue; diseased tissue; myeloid cell disorder; lymphoid cell disorder; bone cartilage tissue growth; tendon tissue growth; ligament tissue growth; nerve tissue growth; regeneration; wound healing; tissue repair; tissue replacement; burn; incision; ulcer; cancer; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New polynucleotides and secreted proteins, useful for treating myeloid or tymphoid cell disorders, in bone cartilage, tendon, ligament and nerve tissue growth or regeneration, in wound healing, and in tissue repair and replacement.
                                                        CAAGGTCCAGTCATCAGATTCTGGCCCAGCGAGAATGGGCTTTTATTGGTGTCCCTTAT
                                                                                                                                                                                                718 CAAGGCCCTGTCATCAAATTCTGGCCCAGGGAAATGGGCCTTCATTGGTGTCCCTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wang J;
Wang D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            J, Zhao QA,
Drmanac RT,
                                                                                                                                                                                                                                                                                                      815 GIGICCCTICIGIGICCCACAAGAAGICGCCAGICAAGAICACG
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Wehrman T, Weng G, Zhou P,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADI21948 standard; cDNA; 1623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel human protein cDNA #207.
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13-SEP-2002; 2002US-00323739.
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Ghosh M, Xue AJ, W
Haley-Vicente D;
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Elashoff MR

Castle AL,

Johnson KR,

Porter MW, GENE LOGIC INC

Mendrick D,

(GENE-)

WPI; 2002-241625/29

02-NOY-2000; 2000US-0244880P. 11-MAY-2001; 2001US-0290029P. 15-MAY-2001; 2001US-0290645P. 22-MAY-2001; 2001US-0295386P. 06-UN-2001; 2001US-0295798P. 13-UN-2001; 2001US-0297457P. 19-UN-2001; 2001US-0298884P. 09-UUL-2001; 2001US-0398884P.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTATTCGAGTGCGCGCTGGGCTTCGTTTGCTAGCAAAGATGGCTGAGGGGGGTTGAGGAAT
                                                                          356 TOGITICCCAGGAGGIATITACCAAAGAICTTTCGGAATGACAGGGGCAGGTTCAAGGCA
                                                                                      416 GIGGIGIGICCIGICTGCAATTACAACGIGCITGGCGTTTATCAAGCCCGCCATCAAC
                                                                                                                                                                                                             536 AGGIGIGACAAIGIGCGIGIGITIAAGCIGGGCCICTICICTGGCCICTGGACTCTG
                                                                                                                                                                                                                                                           GCTCTCTTCTGCTGGATCAGCGACCAAGCCTTCTGTGAGCTGCTCTCCTCCTTTCACTTC
                                                                                                                                                                  476 AATATTTCCCTGATGATTCTGGGACTTCCATGCACTGCGCTGCTTGTTGCAGAGCTGAAG
                                                     Gaps
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differential expression; centrilobular necrosis; steatosis.
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                             DB 10; Length 1623;
     Sequence 1623 BP; 305 A; 457 C; 382 G; 479 T; 0 U; 0 Other;
                                                    IndelB
                            Score 424.2; DB 10;
Pred. No. 3.3e-106;
0; Mismatches 113;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABK62212 standard; cDNA; 595
                               Query Match
Best Local Similarity 81.2%;
Matches 506; Conservative
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The invention relates to methods for predicting toxic effects of compounds or the progression of these toxic effects by determining the compounds or the progression of these toxic effects by determining the global changes in gene expression in unexposed to the coxic class. Also included are methods of predicting at least one toxic effect coils. Also included are methods of a toxic effect, preferably the compound or progression of a toxic effect, preferably the compound compound, comprising detecting the level of expression in a tissue or cell sample exposed to the compound of two or more genes listed in the specification, where differential expression of the genes is indicative of at least one toxic effect or progression. The cresponse and predict cellular pathways that a compound modulates the toxic response and predict cellular pathways that a compound modulates in a cell. The methods utilise a set of at least two probes on a solid support in kit form), where each of the probes comprises a sequence that specifically hybridises to a gene listed in the specification, a computer of specification a database containing information identifying the expression level in a tissue or cell sample exposed to a hepatotoxin of a set of genes comprising at least two genes listed in the specification. The method is useful for elucidating global changes in gene expression and for identifying toxicity markers in the specification. The method is useful for elucidating global changes in gene expression and for identifying toxicity markers in the proper in darkers in the prement and provicity assays. The dense and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3672
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                                                                                                                                                                                                                                                                                                                                                               predicting toxic effects of compounds or the progression of these toxic effects by determining the changes in gene expression in tissues or cells exposed to the toxin and comparing these to gene expression in unexposed tissues or cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sample that has been exposed to a compound or agent. Hepatotoxicity is characterised by centrilobular necrosis and steatosis. The present sequence is an expressed sequence tag (RST) or cDNA derived from a gene which is differentially expressed in response to a hepatotoxic agent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   toxicity markers in drug screening and toxicity assays. The genes and gene expression information may be used as diagnostic markers for the prediction or identification of the physiological state of tissue or or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3557 ATTCTATTGGTTGGATTTCTCAGGAGTCTGGAATCTTCCCTCACGAGTCCTCTTCTCCCAA
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9.6%; Score 400.4; DB 6;
Best Local Similarity 87.9%; Pred. No. 7.2e-100;
Matches 531; Conservative 0; Mismatches 56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; SEQ ID NO 119; 239pp; English.
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                                                CACAGACTIT - - AAAACAIGGCITGIGICTTTCCATACACATCCGGTCAGATTTAAAACT
                                                                                             298 CACAGACTTTAAAAAACAIGGCGTGTGTCTTTCCTACACA---AGTCAGATTTAAAACT
                                                                                                                          ATTTTATAACCACAGAATTAAACCAAGCAAATAGAGTACTTTCAGATATAAACTGTGT
                                  CCAACAACACATCTTTGGCCAGATTGGGATTCTCAATAGATTTTATAGACATTATTCTCC
                                                                                                                                          241 ATTTTATAACTACAATAATTCAACCAAGCAAATAGAGTATTTTTCAGATATATGC--CATT
                                                                                                                                                                       TCATACTTTATGTAGAGTGTGCTATGTATAGGCGGTATGTACCCTGGCTGAAGTAATTT
                                                                                                                                                                                                                                     123 AGTCATTGCTCTGGG-GGATTTACAGATCTTTTGCACTTTATGCTTTTTTTGTGAACTCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 expression profile; hepatotoxicity; liver;
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drug screening; toxicity assay; ds
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2002US-0364045P.
2002US-0364055P.
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15-MAR-2002; 30-DEC-2002;
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of a tissue or cell sample exposed to the compound, and comparing the gene expression profile to a database comprising SEQ ID 1-4925, where differential expression of the gene indicates at least one toxic effect. The method is useful for predicting at least one toxic effect of a compound, predicting hepatotoxicity or the progression of a toxic effect of a compound, identifying an agent that modulates the onset or progression of a toxic response, predicting the cellular pathways that a compound modulates in a cell, and identifying an agent that modulates at least one activity of a protein. The method and compositions of the present invention using a database of genes having liver toxin-induced differential expression, are useful in identifying toxicity markers in liver tissues or cells for drug screening and toxicity assays. Note: The sequence data for this patent did not form part of the printed procession, but was obtained in electronic format directly from WIPO
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                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                              Query Match 9.6%; Score 400.4; DB 10; Best Local Similarity 87.9%; Pred. No. 7.2e-100; Matches 531; Conservative 0; Mismatches 56;
                                                                                                                                                                                                                                                          ftp.wipo.int/pub/published_pct_sequences.
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ADL06640;

The present invention relates to a method for predicting a toxic effect of a compound. The method comprises preparing a gene expression profile

Claim 1; SEQ ID NO 252; 1156pp; English.

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promoting function, polynucleotides encoding the polypeptide and the recombinant process of producing the polypeptide. The present invention also discloses the agonist resisting the polypeptide and its treatment effect. The present invention also discloses the application of the polynucleotides encoding the human protein with 3T3 cell conversion
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  202 OGCAACGIGCITCAACAGCGGCAICIACITAAIAIGGACGCICCIAGIIGIAGIGGGGAI
                                                                                                      ---AGGTGTGACAATGTGCGTGTGTTTAAGCTGGGCCTCTTCTCTGGCCTCT
                                           658 GACCCCCGTGCAGGTGTGACATGCGTGTGTTTAAGCTGGGCCTCTTCTCGGGCCTCT
                                                                                 TCTGCTGGATCAGCGACCAAGCCTTCTGTGAGCTGCTCTCCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 7.8%; Score 323.6; DB 10; Length 1527; Best Local Similarity 73.5%; Pred. No. 2.4e-78; Matches 475; Conservative 0; Mismatches 74; Indels 97;
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                                                                                                                                                                          CCTTTCACTTCCCCTACCTGCACTGTGTGGCATATTCTCATCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                               3T3 cell conversion; promoter; human; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                             Human 3T3 cell conversion promoter PP11646
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        358 AGTCCTTTGGGTTCTGATGTGTGTTTTGGCCATGTGGTTCCCCAGAAGGTATCTACCAAA 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           477
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   598 ACACAGGAAAGGIGGCCAGCAAGGAGGIGGAGACAAGGICTGACGAIGAGIGACICTCTG 657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     promoting function, polymucleotides encoding the polypeptide and the recombinant process of producing the polypeptide. The present invention also discloses the agonist resisting the polypeptide and its treatment effect. The present invention also discloses the application of the polymucleotides encoding the human protein with 3T3 cell conversion promoting function.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               conversion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CATICIGIGGGIICIGAIGIGCITITGGCCAIGIGGIITICCCAGGAGGIAIITACCAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   442 AACGTGCTTGGCGTTTATCAAGCCCGCCATCAACAATATTTCCCTGATGATTCTGGGACT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                              protein with function of promoting 3T3 cell conversion and its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 10; Length 1527;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This invention describes a novel human protein with 3T3 cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1527 BP; 376 A; 357 C; 383 G; 411 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 323.6; DB 10; Length
Pred. No. 2.4e-78;
0; Mismatches 74; Indels
                                                                                                                                                                                                                                                                                          (SHAN-) SHANGHAI XINSHIJIE GENE TECHN DEV CO LTD.
                                    Human 3T3 cell conversion promoter PP11646 cDNA
                                                                      cell conversion; promoter; human; gene; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TCCATGCACTGCGTGCTTGTTGCAGAGCTGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 1; SEQ ID NO 1; 41pp; Chinese.
                                                                                                                                                                                                                    12-SEP-2001; 2001CN-00126725
                                                                                                                                                                                                                                                      12-SEP-2001; 2001CN-00126725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7.8%;
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                                                                                                                                                                                                                                                                                                                                                                                  P-PSDB; ADLO6641
                                                                                                                                                                                                                                                                                                                                                                                                                                       coding sequence
                                                                                                                                                                                                                                                                                                                              Yang S;
                                                                                                            Homo sapiens
                                                                                                                                                CN1403477-A
06-MAY-2004
                                                                                                                                                                                19-MAR-2003
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                                                                                                                                                                                                                                                                               GGTGGACCTIGGCCCTGTTCTGCTGGATCAGTGACCGAGCTTTCTGCGAGCTGCTGTCAT 777
                                                                                                                                                                                                                                                                                                                                                                                                                                forensic; nutritional source; damaged tissue; diseased tissue; myeloid cell disorder; lymphoid cell disorder; bone cartilage tissue growth; tendon tissue growth; ligament tissue growth; nerve tissue growth; regeneration; wound healing; tissue repair; tissue replacement; burn; incision; ulcer; cancer; human; ss; gene; EST; expressed sequence tag.
                                                  CATTCTGTGGGTTCTGATGTGTGCTTTGGCCATGTGGTTTTCCCAGGAGGTATTTACCAAA
                                                                                    GATCTTTCGGAATGACCGGGGTAGGTCAAGGTGGTCAGTGTCCTGTCTGCGGTTAC
                                                                                                                                                                         rctriecacrecacrectearcecaeaecraadeaecareaeaaaccaeceaaeaa
                                                                                                                                                                                                           598 ACACAGGAAAGGTGGCCAGCAAGGAGGTGGACAAGGTCTGACGATGAGTGACTCTCTG
                                                                                                                                                                                                                                       TGGATCTGTCTACTTCCATGCAACGCTGAGTTTCCTGGGTCAGATGCTTGATGAACTTGC
                                                                                                                       AACGTGCTTGGCGTTTTATCAAGCCCGCCATCAACAATATTTCCCTGATGATTCTGGGACT
                                                                                                                                    478 GACGIGCCIGGCAIIIGICAAGCCIGCCAICAACAACAICTCICIGAIGACCCIGGGAGI
                                                                                                                                                                                                                             -----AGGIGIGACAAIGTGCGTGTTTTAAGCTGGGCCTCTTCTCTGGCCTCT
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ou P, Drmanac RT,
                                                                                                                                                                                                                                                                                                 CCTTTCACTTCCCCTACCTGCACTGTGGCATATTCTCATCTG 690
                                                                                                                                                                                                                                                                                                             TCCATGCACTGCGCTGCTTGTTGCAGAGCTGAAG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RW, Ren F, Zhang
Weng G, Zhou P,
                                                                                                                                                                                                                                                                                                                                                                                                               Novel human expressed sequence tag, EST #167.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tang YT, Asundi V, Goodrich RW,
Ghosh M, Xue AJ, Wehrman T, Wen
Haley-Vicente D;
                                                                                                                                                                                                                                                                                                                                                                BP.
                                                                                                                                                                                                                                                                                                                                                             ADI21468 standard; cDNA; 487
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19-SEP-2001; 2001US-0323739P
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                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO2003025148-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
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The invention relates to an isolated polynucleotide encoding a polypeptide with biological activity. The polynucleotides and polypeptides are useful in diagnostics, forenaics, gene mapping, identification of mutations responsible for genetic disorders and other traits, to assess biodiversity, as nutritional sources or supplements. The polynucleotides may also be used as molecular weight markers, chromosome markers or map related gene positions, or as an antigen to raise anti-DNA antibodies, as markers for tissues in which the corresponding polypeptide is expressed, for tissues in which the corresponding polypeptide is expressed, for re-engineering damaged or diseased tissues, for treating myeloid or lymphoid cell disorders, in corresponding to the wound healing, in tissue repair and replacement, in healing of burns, incisions and ulcers, and in treating cancer. The present sequence represents a novel human expressed sequence tag, EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                               New polynucleotides and secreted proteins, useful for treating myeloid or lymphoid cell disorders, in bone cartilage, tendon, ligament and nerve tissue growth or regeneration, in wound healing, and in tissue repair and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                249
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                                                                                                                                                                                                                                Example 2; SEQ ID NO 719; 156pp; English.
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2003-354603/33
                        P-PSDB; ADI21688
                                                                                                                                                                           replacement
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(AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the
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Chen R, V
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ao QA, Wang D, Wang J, Zhang J, Ren F,
Yang Y, Wejhrman T, Goodrich R,
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2000US-00560B75.

2000US-00598075.

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P-PSDB; AAM78433.
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'Yang Y,
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Ma Y, zh
Xue AJ,
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                                                                                                                                                                                                                                 The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to production of other cytokines or cell differentiation or which may induce polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, nematopolesis regulating activity, tissue growth factor activity, immunomodulatory activity and activity and may be useful in the diagnosis and/or readment of cancer, leukaemia, nervous system disorders, arthritis and inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111 from the sequence listing were missing at the time of publication
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    Chen R,
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    Ren F,
    Wang J, Zhang J,
1 T, Goodrich R;
                                                                                                                                                                                          Claim 1; Page 4462; 6221pp; English.
    Wang D, Wang
Wejhrman T,
                                                                                                                                                    diagnosis and gene therapy
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Matches 437; Conservative
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10, Appli
5, Appli
5, Appli
5, Appli
6, Appli
45, Appl
2955, A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 11241, Application US/09621976

Sequence 11241, Application US/09621976

GERERAL INFORMATION:
APPLICANT: Unusa Milne Edwards, J.B.
APPLICANT: Jobert, S.
APPLICANT: Gloradano, J. Y.
TITLE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 2.7%; Score 114.2; DB 4;
Best Local Similarity 90.4%; Pred. No. 2.1e-25;
Matches 122; Conservative 0; Mismatches 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 14, Application US/08232463
; Batent No. 5670367
; GENERAL INFORMATION:
   APPLICANT: DORNER, F.
; APPLICANT: SCHEIFLINGER, F.
; APPLICANT: FALKNER, F. G.
; TITLE OF INVENTION: RECOMBINANT FOWLEOX VIRUS
; NUMBER OF SEQUENCES: 52
; CORRESSEER: FOLEY & Lardner
; ADDRESSEE: FOLEY & Lardner
; STREET: 1800 Diagonal Road, Suite 500
US-09-149-476-90
US-08-920-422-17
US-08-921-064-126
US-09-790-988-1
US-08-951-924A-1
US-09-172-339-3
US-09-172-339-3
US-09-245-041-5
US-09-245-041-5
US-09-245-041-5
US-09-589-238-5
US-09-589-238-5
US-09-513-999C-923
US-08-150-331-45
US-08-150-331-45
US-08-150-331-45
US-08-150-331-45
US-08-150-331-45
US-08-150-331-45
US-08-150-331-45
US-09-270-767-13559
US-09-310-185-157
US-09-310-085-157
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NAME/KEY: promoter
LOCATION: (1)..(1141)
OTHER INFORMATION: consensus sequence of A.t., L.a., and B.n. FAE1 promoters
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2195 AGAGTTTTTAAATGAATAGACTTCATTCTGCTTTTGTGGCTTTGGAGTTTTAAAAGTAAC 2254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TTGCTGGGCTATTTCTTGTTTATAGTCACAAATATTTATAGAACATGAAGGTGTAAAATA 2314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2435 TACTGTAGCTTAAAATATGTTTAAA-ATGACTTTGAGTGAAATGTTTGTGGCAACCTAGG 2493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2494 GGTTTATGGATCAGAATTGCGGCTGAGTCCTTTGGTTTTTGAGTCTAGAAGTTTTCAGAG 2553
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 175 WDDDTKYHMWNNNGCBTVTWMVRYKTDRDWSBKRMNYGMBWWKNWSYDVTYYWWVWDDMC 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               235 KRKVRRWVRTRGRMRNYMVAWBTAHRRRYNNGWTBAMAYRRWTMINININAKAMCKRAKY 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            295 WGWNRABVNSTCTIWKSKTIKVRISCWANNCRAGDANKDHKWWKWSAAMGVYWNNNNNN 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15 ::::: | : ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: |
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              655 ATCARDDYYAASRWYAMANAKWYYYKBAANNAYYTHANNWWGCWNNATDTRRTMWKNNNN 714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              715 NNAGTWKNNNNNAKNASAAKNYAAAVKAAKKHWRWANKWAMRGWHADAAABTTDKRNN 774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2315 AGTTGTCTTTTATTAAATTCATAGCATTTACCAACTCTCCCAGGTAGCAAACACAGGTC
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                                                                                                                                     GENERAL INFORMATION:
APPLICANT: The University of British Columbia
APPLICANT: The University of British Columbia
TITLE OF INVENTION: Regulation of Embryonic Transcription in Plants
FILE REFERENCE: 4810-58741
CURRENT APPLICATION NUMBER: US/09/806,708B
CURRENT FILING DATE: 2001-04-03
PRIOR FILING DATE: 1999-08-04
NUMBER OF SEQ ID NOS: 23
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
1.1%; Score 46; DB 4; Length 1141;
Best Local Similarity 9.9%; Pred. No. 0.0022;
Matches 75; Conservative 280; Mismatches 405; Indels
                                                                    ; Sequence 22, Application US/09806708B; Patent No. 6784342
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                                      JS-09-806-708B-22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               720 TCGCCTACTITGATGCTGCCTCAGAGATACCTGAGCAAGGTCCAGTCATCAGATTCTGGC 779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     480 TITCCCTGATGATTCTGGGACTTCCATGCGCTGCCTGCTTGTTGCAGAGCTGAAGAGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   540 GTGACAATGTGCGTGTGTTTAAGCTGGGCCTCTTCTCTGGCCTCTGGTGGACTCTGGCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 660 ACCIGCACTGIGIGGCATATICTCATCTGCCTTGGTACCTGGGCTGTGTGTGTGTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        780 CCAGCGAGAAAIGGGCTTTTATTGGTGTCCCTTATGTGTCCCTTCTGTGTGCCCCACAAGA
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Matches 36; Conservative 222; Mismatches 189; Indels
                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMMU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1.3%; Score 55.8;
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                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIPICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE:
                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
PILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (703)836-9300
(703)683-4109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                     COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TOPOLOGY: linear; IMMEDIATE SOURCE: ; CLONE: pTZgpt-Fl8 US-08-232-463-14
Alexandria
                                                                                                      22313-0299
                                                                    USA
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JS-09-621-976-2813
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                128 ATGATTATACCTCCAATGTTC--GGTGCAATTCAGAGTGTTAGAGACGGTCTGGAAAAGC 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     221 GGCATCTACTTAATATGGACGCTCCTAGTTGTAGTGGGGGATTGGATCTGTCTACTTCCAT 280
: : : : : : : : | 334 | 334 | 335 | 337 | 334 | 334 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              186 GGTACATTGCTTCTTATTTAGCACTCAC-AGTGGTAGGAATGGGATCCTGGTGCTTCCAC 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  70
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             245 ATGACTCTGAAATATGAAATGCAGCTATTGGATGAACTCCCAATGATAT 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 45.4; DB 4; Length 1063; Pred. No. 0.0031;
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                                                                                                               2854 GGCAGGCAAAACATTTATACATGTAACGTAATAAATGCATA 2894
                                                                                                                                                      APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: No. 6783969el Nucleic Acids and
TITLE OF INVENTION: POlypeptides
FILE REPERBUGE: 803
CURRENT APPLICATION NUMBER: US/09/799,451
CURRENT FILING DATE: 2001-03-05
NUMBER OF SEQ ID NOS: 948
SOFTWARE: Dt_FL_genes Version 2.0
                                                                                                                                                                                                                                                                                                                                                                      Sequence 875, Application US/09799451
Patent No. 6783969
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Yamazaki, Victoria
Chen, Rui-hong
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Zhao, Qing A.
Wang, Jian-Rui
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APPLICANT: Zhou, Ping
APPLICANT: Goodrich, Ryle
APPLICANT: Asundi, Vinod
APPLICANT: Ren, Feiyan
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Ghosh, Reena
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ORGANISM: Homo sapiens
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; LOCATION: (2)..(802)
US-09-799-451-875
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Best Local Similarity
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Wang,
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US-09-799-451-875
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SEQ ID NO 875
LENGTH: 1063
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APPLICANT:
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3860 TIAAAACAIGGCIIGICITIICCAIACACAICCGGICAGAIIIAAAACTAIIITAIAAC 3919
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3800 ACATCTTTGGCCAGATTGGGATTCTCAATAGATTTTATAGACATTATTCTCCCACAGACT 3859
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           188 GKARKWSTWRKSRSYASARSAKRCCYSCSWGAMSWKYMWRMWRMRGWATGAGMKAWRASC 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            68 YKKXAMCRIKIKKKKKKKGYMMMYWGWRRSYMAMWIRIWIGYAYYRSMMYWRYRCWKKK 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       308 KRWWWCWARMYRYSTGTRASMWWRRWYYTWMKKWWKYAWARAARAWRWWAMWRAKACAAA 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              248 MMRRKYAGKSKTSYKSMWMCWTRSWKYCYTKARWTGYYCYRKGGMWGKRGRWYASKKYMW 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          128 AYYRKTTCYSSKGWTWWKRWKKAMTTWWWKKTYYWAATRYWWMMCWTKRWRASWWYCWWW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11 WYAKCWIKWKWSWSYWMYWKWYYMKTYWRWRRKKKKAWWKYWKIWTWWYW---RYAMWGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3980 IGTAGAGIGIGCTAIGTATAGGCGGIAIGTACCCIGGCIGAAGIAAIAITAACCATAGCI
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1.1%; Score 44.8; DB 4; Length 8
Best Local Similarity 12.0%; Pred. No. 0.004;
Matches 44; Conservative 171; Mismatches 148; Indels
Sequence 2813, Application US/09621976
Patent No. 6639063
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Johert, S.
APPLICANT: Glordano, J.Y.
TITLE OF INVENTION: ESTS and Encoded Human Proteins.
PILE REFERENCE: GENSET.054PR2
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APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: ESTS and Encoded Human Proteins.
FILE PEFERENCE: GENEST. 054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SEOFTWARE: Patent.pm
SEO ID NO 2813
LENGTH: 832
                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 2813
LENGTH: 832
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Homo sapiens
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US-09-621-976-2813
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US-09-621-976-2813/c
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NAME/KEY: misc feature
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APPLICANT: Hong Zhang
APPLICANT: Jacqueline Wyatt
TITLE OF INVENTION: ANTISENSE MODULATION OF BH3 INTERACTING DOMAIN DEATH AGONIST
TITLE OF INVENTION: EXPRESSION
FILE REFERENCE: RTS-0135
CURRENT APPLICATION NUMBER: US/09/657,346A
CURRENT APPLICATION NUMBER: 2000-09-07
NUMBER OF SEQ ID NOS: 174
SEQ ID NO 96
LENGTH: 30310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2781 CAGCAACTCCAGCCCTGGGGCATCTGACGCCCTCTTCTGACTTCTAAGGGCATTTGGTGC 2840
                                                                                                                                                                              2085 TTCTGAGTGGTGTCCTGAGTCTGAAGGAGCTAGCTGGGGGTTCTGGCCACTTCTAGGATCT 2144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2145 CTTACTCTGTTTAGAACCTTCACAGGGTACAAAGTGGGAACTGGACTTAAAGAGTTTTTA 2204
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                                                                                                                                                                                                                                                                                                                                                                                                                   2265 ATTICTIGTITAIAGICACAAAIAITITAIAGAACAIGAAGGIGIAAAAIAAGITGICTIT 2324
                                                                                                                                                                                                    360 WIWWKIWWYWITYIWIRMWMKKKARRWYYWKSIYACASRYRKYIWGWWWYWKRMMSI 301
                                                                                                                                                                                                                                                                              300 RWYCYMCWKCCMYRGRRCAWYTWARGRWWSYAWGKWKSGMRSAMSMCTRNYYKKGSTYWTM 241
                                                                                                                                                                                                                                                                                                                                                            240 KCTCATWCYWYWKYWKRWWSKICWSGSRGGYMISYTSTRSYSMYWASWMYTWCWWMGRWW 181
                                                                                                                                                                                                                                                                                                                                                                                                                                          122 YRYWWRKKSYRRTRCAMAYAWKTKRSYYWCWRWKWKRCMMMMMAMAYGKTMMMRACWKT 63
                                                                                                                                           Gaps
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                                                                                                Query Match
Best Local Similarity 12.7%; Pred. No. 0.023;
Matches 43; Conservative 156; Mismatches 137; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2385 CGATTTACAAGGCAGGAATACTTGGTTTTGAATGATTG 2422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62 RYWRWWAWAMWRWWTMMMYYWYWRAMKRRWWRKWR 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-657-346A-96
; Sequence 96, Application US/09657346A
; Patent No. 6503754
; GENERAL INFORMATION:
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NAMBY KRX: CDS
LOCATION: (27235)...(27246)
US-09-657-146A-96
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CDS
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CDS
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NAME/KEY: CDS
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; FEATURE:
; NAME/KEY: CDS
; LOCATION: 235..399
US-09-621-976-2813
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NAME/KEY: C
LOCATION:
NAME/KEY: C
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173 YNYSYNYNYSYNYNYSYNYNYSYNYNYSYNYNYSYNYNYSYNYNYSYNYNYSYN 114
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                                                                                                                                                         Sequence 17. Application US/09007005B

Sequence 17. Application US/09007005B

Sequence 17. Application US/09007005B

GENERAL INPORMATION:
APPLICANT: Szostak, Jack W.
APPLICANT: Liu, Rihe
TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN
TITLE OF INVENTION: FUSIONS
FILE REFERENCE: 00786/350003
CURRENT FILING DATE: 1998-01-14
EARLIER APPLICATION NUMBER: 60/035,963

EARLIER FILING DATE: 1997-01-27
EARLIER FILING DATE: 1997-01-66

NUMBER OF SEQ ID NOS: 33

SOFTWARRE: PSECSEC for Windows Version 4.0

LENGTH: 289
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APPLICANT: SCORGAK, Jack W.
APPLICANT: SCORGAK, Jack W.
APPLICANT: Roberts, Richard W.
APPLICANT: Liu, Richard W.
APPLICANT: Liu, Riberts, Richard W.
TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN TITLE OF INVENTION: PUSIONS; FILE REFERENCE: 00706/350007; CURRENT FAPPLICATION NUMBER: US/09/244,796; CURRENT FILING DATE: 1999-02-05; EARLIER APPLICATION NUMBER: 60/035,963; EARLIER PILING DATE: 1997-01-27; EARLIER PILING DATE: 1997-01-27; EARLIER RILING DATE: 1997-01-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 1.0%; Score 41; DB 3; Length 289; Best Local Similarity 7.6%; Pred. No. 0.026; Matches 17; Conservative 97; Mismatches 111; Indels
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Patent No. 6281344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | LOCATION: (1) ... (289)
| OTHER INFORMATION: n = A,T,C or G
US-09-007-005-17
TYPE: RNA
ORGANISM: Artificial Sequence
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2431 ATTITACTGTAGCTTAAAATATGTTTAAAATGACTTTGAGTGAAATGTTTGTGGCAACCT 2490
                                                       2371 AGICATITGATIGGCGATITACAAGGCAGGAATACTIGGTTTTGAATGATTGTATATGTC 2430
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                                                                                                   210 TTCCARIARTITACGCARIARAGATTCATCTAGATCARTATATTTTCTCTTTTRATTTTAR 151
     270 AATATCTTGATAATTTATAATTTGATTAATATTTTCAAAATCTATAGTAATTAAAGTCAA 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Gilbert, Michel
APPLICANT: Gilbert, Mararchuk, Warren W.
APPLICANT: Wakarchuk, Warren W.
APPLICANT: Wakarchuk, Warren W.
APPLICANT: Wakarchuk, Warren W.
APPLICANT: National Research Council of Canada
TITLE OF INVENTION: Campylobacter Giycosyltransferases for Biosynthesis of
TITLE OF INVENTION: Gangliosides and Ganglioside Mimics
FILE REFERENCE: 019633-0001100S
CURRENT APPLICATION NUMBER: US/09/495,406
PRIOR PELICATION NUMBER: US 60/118,213
PRIOR PILING DATE: 1999-02-01
NUMBER OF SEQ ID NOS: 35
SOFTWARE: Astentin Ver. 2.1
LENGTH: 1044
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OTHER INFORMATION: transferase from C. jejuni strain OH4384 (ORF 5a
OTHER INFORMATION: of LOS biosynthesis locus)
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                                                                                                                                                                                                                                                            2491 AGGGGTTTATGGATCAGAAT 2510
                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 12, Application US/09495406; Patent No. 6503744; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                           AATGGAAAGGATAAGAGAAT 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA ORGANISM: Campylobacter jejuni
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        . (1044)
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LOCATION: (1)
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APPLICANT: Keith Weinstock et al
APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
TITLE OF INVENTION: POR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.13
CURRENT APPLICATION NUMBER: US 60/074,725
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR FILING DATE: 1998-02-13
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 6940
LENGTH: 435
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; OTHER INFORMATION: Identity of nucleotide sequences at the above locations are unkno
US-09-248-796A-6940
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        173 YNYSYNYNYSYNYNYSYNYNYSYNYNYSYNYNYSYNYNYSYNYNYSYNYNYSYN 114
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                                                                                                                                                                                                                                                                                                                                                                                                          ; Score 41; DB 3; Length 289; Pred. No. 0.026; 97; Mismatches 111; Indels
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SARLIER FILING DATE: 1998-01-14
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PastSEQ for Windows Version 4.0
                                                                                                                                                                                                     FEATURE: OTHER INFORMATION: Translation template
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; Sequence 6940, Application US/09248796A
; Patent No. 6747137
                                                                                                                                                                                                                                                                                                      ; LOCATION: (1)...(289)
; OTHER INFORMATION: n = A,T,C or G
US-09-244-796-17
                                                                                                                                                                                                                                                                                                                                                                                                       ch 1.0%; 1.0%; 1 Similarity 7.6%; 1 17; Conservative 9
                                                                                                                                                                          ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                 NAME/KEY: misc feature
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                                                                                              SEQ ID NO 17
LENGTH: 28
                                                                                                                                                     TYPE: RNA
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                                                                                                                                                                                                                                                       FEATURE:
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US-09-495-406-1/c
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                                                                                                                 GENERAL INPORMATION:
GENERAL INPORMATION:
GENERAL INPORMATION:
APPLICANT: Gibbert, Michel
APPLICANT: Gibbert, Michel
APPLICANT: Makarchuk, Warren W.
TITLE OF INVENTION: Campylobacter Glycosyltransferases for Biosynthesis of
TITLE OF INVENTION: Gangliosides and Ganglioside Mimics
TITLE OF INVENTION: Gangliosides and Ganglioside Mimics
FILE REFERENCE: 019633-00041103
CURRENT APPLICATION NUMBER: US/09/816,028A
CURRENT APPLICATION NUMBER: US 60/118,213
PRIOR APPLICATION NUMBER: US 60/118,213
PRIOR FILING DATE: 2000-01-31
NUMBER OF SEQ ID NOS: 49
SOFFWARE PARENT PAREN
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Patent No. 6723545
GENERAL INFORMATION
GENERAL INFORMATION
APPLICANT: Gilbert, Michel
APPLICANT: Wakarchuk, Warren W.
APPLICANT: National Research Council of Canada
APPLICANT: National Research Council of Canada
TITLE OF INVENTION: Campylobacter Glycosyltransferases for Biosynthesis of
TITLE OF INVENTION: Campylobacter Glycosyltransferases
FILE REFERENCE: 019633-000111US
CURRENT APPLICATION NUMBER: US/10/303,162
CURRENT FILING DATE: 2002-11-21
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OTHER INFORMATION: beta-1,4 N-acetylgalactosaminyl (GalNAc)
OTHER INFORMATION: transferase from C. jejuni strain OH4384 (ORF 5a OTHER INFORMATION: of lipooligosaccharide (LOS) biosynthesis locus)
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US-09-816-028A-16/c
; Sequence 16, Application US/09816028A
; Patent No. 6699705
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APPLICANT: Gilbert, Michel
APPLICANT: Gilbert, Marren W.
APPLICANT: National Research Council of Canada
TITLE OF INVENTION: Campylobacter Glycosyltransferases for Biosynthesis of
TITLE OF INVENTION: Gangylobacter Glycosyltransferases for Biosynthesis of
TITLE OF INVENTION: Gangylobacter Glycosyltransferases for Biosynthesis of
TITLE OF INVENTION: Gangylobacter Glycosyltransferases for Biosynthesis of
TITLE OF INVENTION NUMBER: US/09/495,406
CURRENT APPLICATION NUMBER: US 60/118,213
PRIOR FILING DATE: 1999-02-01
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COTHER INFORMATION: beta-1,4 N-acetylgalactosaminyl (GalNAc)
OTHER INFORMATION: transferase from C. jejuni strain OH4384 (ORF 5a)
COTHER INFORMATION: of lipooligosaccharide (LOS) biosynthesis locus)
US-10-303-162-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1.0%; Score 40; DB 4; Length 1044;
45.7%; Pred. No. 0.16;
tive 0; Mismatches 165; Indels
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OTHER INFORMATION: including LOS biosynthesis locus
PRIOR APPLICATION NUMBER: US/09/816,028
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: US 60/118,213
PRIOR PILING DATE: 1999-02-01
PRIOR FILING DATE: 2000-01-31
PRIOR FILING DATE: 2000-01-31
NUMBER OF SEQ ID NOS: 49
SOFTWARE: PatentIn Ver: 2.1
SEQ ID NO 16
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Patent No. 6503744
GENERAL INFORMATION:
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ORGANISM: Campylobacter jejuni
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Best Local Similarity 45.7
Matches 139; Conservative
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SOFTWARE: Patentin Ver. 2.1
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APPLICANT: Gilbert, Michel
APPLICANT: Makarchuk, Warren W.
APPLICANT: Nakarchuk, Warren W.
APPLICANT: National Research Council of Canada
TITLE OF INVENTION: Campylobacter Glycosyltransferases for Biosynthesis of
TITLE OF INVENTION: Gangliosides and Ganglioside Mimics
TITLE OF INVENTION: Gangliosides and Ganglioside Mimics
TITLE OF INVENTION: Gangliosides and Ganglioside Mimics
CURRENT APPLICATION NUMBER: US 60/118,213
PRIOR FILING DATE: 2001-03-21
PRIOR FILING DATE: 1999-02-01
PRIOR PELICATION NUMBER: US 60/118,213
PRIOR FILING DATE: 2000-01-31
PRIOR FILING DATE: 2000-01-31
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1
LENGTH: 11474
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                                            1.0%; Score 40; DB 4; Length 11474;
45.7%; Pred. No. 1.2;
tive 0; Mismatches 165; Indels (
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1.0%; Score 40; DB 4; Length 11474;
Best Local Similarity 45.7%; Pred. No. 1.2;
Matches 139; Conservative 0; Mismatches 165; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application US/09816028A Patent No. 6699705
GENERAL INFORMATION:
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ORGANISM: Campylobacter jejuni
                                       Query Match
Best Local Similarity 45.77
Matches 139; Conservative
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JS-09-495-406-1
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Search completed: November 21, 2004, 07:04:46 Job time : 360.166 Becs

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November 20, 2004, 20:53:12; Search time 1950.22 Seconds (without alignments) 11567.962 Million cell updates/sec
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| cgn2_6/ptodata/2/pubpna/US07_NEW PUB.seq:*
| cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
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GenCore version 5.1.6
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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		Description		Sequence 1, Appli	Sequence 21, Appl	Sequence 151, App	Sequence 3, Appli	Sequence 6, Appli	Sequence 119, App	Sequence 48, Appl	Sequence 4, Appli	Sequence 2618, Ap	Sequence 2618, Ap	Sequence 611, App	Sequence 50197, A
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SUMMAKIES		ar		US-10-017-410-1	US-10-188-832-21	US-10-295-027-151	US-10-017-410-3	US-10-182-447-6	US-09-917-800A-119	US-09-945-527-48	US-10-182-447-4	US-10-172-118-2618	US-10-342-887-2618	US-10-106-698-611	US-10-242-535A-50197
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		Query Match Length DB I		4175	4202	4212	828	822	595	744	792	1098	1098	1473	418
	œ	Query Match		100.0	17.3	17.3	15.9	15.7	9.6	7.9	4.2	3.1	3.1	3.0	1.6
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13 65 1.6 418 14 63.6 1.5 57530 15 58.2 1.4 35425 17 58.2 1.4 35425 19 52.6 1.3 19609 20 49.4 1.2 10234 22 48.6 1.2 10234 24 47.6 1.2 10234 25 47.6 1.1 50657 28 47.6 1.1 50657 29 47.4 1.1 50657 29 47.4 1.1 50657 29 47.6 1.1 32495 31 46.6 1.1 171936 32 46.6 1.1 171936 34 45.6 1.1 171936 35 45.6 1.1 171936 36 45.6 1.1 171936 37 45.6 1.1 171936 38 45.6 1.1 171936 39 45.6 1.1 171936 31 45.6 1.1 171936 32 46.7 1.1 171936 33 45.7 1.1 171936 34 45.7 1.1 171936 35 45.7 1.1 171936 36 45.7 1.1 171936 37 45.7 1.1 171936
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ALIGNMENTS

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Sequence 1, Application US/10017410
Publication No. US20020115094A1
GENERAL INFORMATION
APPLICANT: Farnham, Peegy J
APPLICANT: Farnham, Peegy J
APPLICANT: Farnham, Polynucleotide Differentially Expressed in Liver Cancer
TILLE REFERENCE: 960296,970ucleotide Differentially Expressed in Liver Cancer
CURRENT APPLICATION NUMBER: US/10/017,410
CURRENT FILING DATE: 2001-12-14
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin Ver: 2.1
SEQ ID NO 1
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                                                                                                                                                                                                                                                                                     LENGTH: 4175
TYPE: DNA
ORGANISM: Mus musculus
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NAME/KEY: CDS
LOCATION: (35)..(859)
US-10-017-410-1
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Db 1201 CTCAACCCCTGATAAACAAGACCTTCTGATTTGGTGATGAAAGGTTCCAGAACTTTTCA Qy 1261 TTTTGCCGGGAGAAACTGTCCTTCAACAAAACCAAGTGGGCAAAAACACGTGTGGGGGGGTG Db 1261 TTTTGCCGGGGAGAAACTGTCCTTCAACAAAACCAAGTGGGCAAAACACGTGTGGGGGGGTG	1321 T 1321 T	1381	1441	Oy 1501 TTCTGCTCTTCCAGAGTGCAGCAGCCCACAGAGAATCCTTCAGGTTATGTGAA	Qy 1561 GATTCCACACACACCCCCTCTTGTGACCTCTGTGAGCAAGGCCTCGTTGTAATCGCG	Oy 1621 GAGGCAGCTCTGAGGGCTCACTGTGGAGGCGCCTGTGAGATTTTGGAAAGCTTTTCTTA	Qy 1681 TIGGAAGCTTTIGGIGIGIGIGIGIGIGIGIGIGIGIGIGIGIGIG	QY 1741 AGGGGATATGTCTCCTGAGTGACGTAGCCTCCCTAGGATGTGGGCCTCCGGCTTTTGT	QY 1801 TICADABACCIGGIGCTBACTGGITTCTCAGAGCACTITGCICTTCTTGATGCTGGGC DD 1801 TICADABACCIGGIGCTBACTGGITTCTCAGAGCACTITGCICTTCTTGATGCTGGGGC	QY 1861 GGTCACTACACTCTGATTGGCTGGCGGATCCCAGGGAGGAGGAGGACTCTGACA	Qy 1921 TGAATGTCTCTCACCTGCATCCTACTGTCTTCAGGCTCTTTCAGGGTATGAAGTGG	OY 1981 GTATGGGGTATCTCAGGGATGTTTGTAACTCAGGCACCTTCTGCTTTCTGACATTCCATT	Qy 2041 GTCAGTGAGACTGCACTCAGGGACTTGGAACACCGTTCTGAGTGGTGTCCT	Qy 2101 GAGTCTGAAGAGCTAGCTGCGGGTTCTGGCACTTCTAGGATCTCTTACTCTGTTTAGAA	OY 2161 CCTTCACAGGGTACAAAGTGGGAACTGGACTTAAAAGAGTTTTTAAATGAATAGACTTCAT	Oy 2221 TCTGCTTTTGTGGCTTTGAAGTATTTAAAGTAACTTGCTGGGCTATTTCTTGTTTATAGT	Qy 2281 CACAAATATTTATAGAACATGAAGGTGTAAAATAAGTTGTCTTTTATTAAATTCATAGCA
	41 GCTCCTAGTTGTAGTGGGGATTGGATCTGTCTACTTCCATGCAACGCTGAGTTTCCTGGG	301 TCAGATGCTTGATGAACTTGCCATTCTGTGGGTTCTGATGTGCTTTGGCCATGTGGTT 360	361 TCCCAGGAGGTATTTACCAAAGATCTTTCGGAATGACAGGGCAGGTTCAAGGCAGTGGT 420 	421 GTGTGTCCTGTCTGCAATTACAACGTGCTTTATCAAGCCCGCCATCAACAATAT 480 	TTCCCTGATGATTCTGGGACTTCCATGCACTGCCTGCTTGCT	TGACANTGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	CTTCTGCTGGATCAGCGACCAAGCCTTCTGTGAGCTGCTCTCCTTTCACTTCCCCTAACCTACCCTAACCTACCT	CITCIGCIGGAICAACGACCAAGCCIICIGGAAGCIGCICICCIICIGCATICACTIC CCTGCACTGTGTGTGGCATATTCTCATCTGCTTTGTTTCGTTCG	CGCCTACTTTGATGCTGCCTCAGAGATACCTGAGCAGGTCGTACCTGGGGTTGCTACCTAGCTAG	CGCCIACI I GAIGCITTATIAGAATIACCIGAGGAAGGICCAGICAGAICC CGGGGGAAAAGGGGTTTATIAGGGTGCCCCAG	41 GTCGCCAGTCAAGATCACGTGATGCAAGGCAGTGACCAGCTTCTCTACTTACT	CGAGTGCGCCGCTGCGTTTGCTAGCAAGATGCTGACGTTCTGTTTTGTTTG	61 TGGTGTGGGGTGTTTAAAATTCTGCTCCTTTGTGATCTAACTGGACCACTGTGCCTGACCT		81 ATACGGGCTTGCTGGGTTATGTCCATAATGACATCAACAGGGTAGTTCTTTGGGAGGACCT	41 AGGGCAACCCAAAGTTCTTGCTGGAAGGGCACCTCCAACAGGTAGTTCTTTGGGAACCCT 41 AGGGCAACCCAAAGTTTCTTGCTGGAAGGGTAGCTTGCTGTTTCCACCATTTCCAGGCTTTCCAAGATTTCTTTTTTTT	1141 AGGGCAACCCAAAGTTTCTTGCTGGAGAGGTAGCTTGCTGTTTCCACCATTTCCAGGGT 1200 1201 CTCAACCCCCTGATAAACAAGACCTTCTGATTTGGTGATGAAAGGTTCCAGAACTTTTCA 1260

The control of the	3421 CTTCTGTCTGCTTCCCTTTGTAATGTGATCCACTCGGGGAAATGGGTGTCTACCCAGGGA 3480 3481 AAAGTGCTACCCTTTGTAATGTGATCCACTCGGGGAAATGGGTGTCTACCCAGGGA 3480 3481 AAAGTGCTACCCCATCACGGGTCAACACTGGTTGAACTCAACCCAGGGA 3480 3481 AAAGTGCCTACCCCACTCACGGGTCAACAGTTGTTGAACTACACACAGGGTTGTTGTTGATTGA	3961 4021 4021 4021 4081 4081 4181 4181 4181 4181 4181 418
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Sequence 151, Application US/10295027
Sequence 151, Application US/10295027
Publication No. US20032335041
Sequence 151, Application No. US20032335041
SAPELCANT: Air, Daniel
APPLICANT: Ginsberg, Wendy M.
APPLICANT: Ginsberg, Wendy M.
APPLICANT: Ginsberg, Wendy M.
APPLICANT: Ginsberg, Wendy M.
APPLICANT: Ginsberg, Wendy M.
APPLICANT: Ginsberg, Wendy M.
APPLICANT: Murray, Richard
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APPLICANT: Murray, Richard
APPLICANT: Murray, Richard
APPLICANT: Methods of Screening for Modulators of Cancer
CURRENT FILING DATE: 2002-11-13
PRIOR APPLICATION NUMBER: US 60/350,666
PRIOR APPLICATION NUMBER: US 60/330,394
PRIOR PRING DATE: 2001-11-21
PRIOR APPLICATION NUMBER: US 60/34,393
PRIOR PELING DATE: 2001-11-21
PRIOR APPLICATION NUMBER: US 60/34,393
PRIOR PELING DATE: 2001-11-21
PRIOR APPLICATION NUMBER: US 60/34,393
PRIOR PELING DATE: 2001-11-21
PRIOR APPLICATION NUMBER: US 60/34,393
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PRIOR APPLICATION NUMBER: US 60/34,349
PRIOR PELING DATE: 2002-01-10
PRIOR PELING DATE: 2002-01-10
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PRIOR PELING DATE: 2002-01-10
PRIOR PELING DATE: 2002-01-10
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84.9%; Pred. No. 6e-200;
ive 0; Mismatches 142; Indels
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Best Local Similarity 84.9
Matches 823; Conservative
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; ORGANISM: Homo sapiens
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PRIOR APPLICATION NUMBER: US 60/350,666
PRIOR FILING DATE: 2001-11.13
PRIOR APPLICATION NUMBER: US 60/372,246
PRIOR FILING DATE: 2002-04-12
NUMBER OF SEQ ID NOS: 207
SOFTWARE: Patentin Ver. 2.1
LENGTH: 4202
                                                                                                                                                                              ; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-188-832-21
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                                                                                                           DB 13;
                                                                                                          Score 664.8; DB 13;
Pred. No. 3.8e-183;
0; Mismatches 102;
                                                                                                          Query Match
Best Local Similarity 87.7%;
Matches 726; Conservative
2.1
                                                                         .. (825)
SOFTWARE: Patentin
SEQ ID NO 3
LENGTH: 828
                                TYPE: DNA
ORGANISM: Homo
                                                               ; NAME/KEY: CDS
; LOCATION: (1)
US-10-017-410-3
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Publication No. US20020115094A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Farnham, Peggy J
APPLICANT: Graveel, Carrie R
TITLE OF INVENTION: Polynucleotide Differentially Expressed in Liver (
CURRENT APPLICATION NUMBER: US/10/017,410
CURRENT FILING DATE: 2001-12-14
NUMBER OF SEQ ID NOS: 4
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                                                                                                                                               GIGICCCTICIGIGCCCACAAGAAGICGCCAGICAAGAICACG 859
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APPLICANT: Castle, Arthur
APPLICANT: Castle, Arthur
APPLICANT: Elashoff, Michael
APPLICANT: Elashoff, Michael
APPLICANT: Gaene Logic, Inc.
TITLE OF INVERTION: MOLECUlar Toxicology Modeling
FILE REFERENCE: 44921-5038-US
CURRENT APPLICATION NUMBER: US 60/222,040
PRIOR APPLICATION NUMBER: US 60/222,040
PRIOR FILING DATE: 2000-07-31
PRIOR FILING DATE: 2000-07-31
PRIOR PELICATION NUMBER: US 60/290,029
PRIOR PELICATION NUMBER: US 60/290,645
PRIOR FILING DATE: 2001-05-15
PRIOR FILING DATE: 2001-05-15
PRIOR FILING DATE: 2001-06-15
PRIOR FILING DATE: 2001-06-06
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PRIOR FILING DATE: 2001-07-09
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; Sequence 119, Application US/09917800A
; Patent No. US20020119462A1
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 119
LENGTH: 595
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Sequence 6, Application US/1018247
Publication No. US20030185814A1
GENERAL INFORMATION:
APPLICANT: HOFMANN, KAY
APPLICANT: RADT, MARCUS
TILLE OF INVENTION: CERAMIDASE
FILE REFERENCE: P66055U30
CURRENT APPLICATION NUMBER: US/10/182,447
CURRENT FILING DATE: 2002-07-29
PRIOR FILING DATE: 2001-01-27
PRIOR FILING DATE: 2001-01-27
PRIOR FILING DATE: 2000-01-27
PRIOR FILING DATE: 2000-01-27
PRIOR FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: DE 1001392.31
PRIOR FILING DATE: 2000-01-27
PRIOR FILING DATE: 2000-01-27
PRIOR FILING DATE: 2000-01-27
PRIOR FILING DATE: 2000-01-37
PRIOR FILING DATE: 2000-01-37
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PARENTIN Ver. 2.1
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US-10-182-447-6
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Best Local Similarity
Matches 725; Conserv
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                           494 CTGGGACTTCCATGCACTGCGCTGCTTGTTGCAGAGCTGAAGAGGTGTGACAATGTGCGT
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al Similarity 52.6%; Score 174.8; DB 15; Length
al Similarity 52.6%; Pred. No. 1.2e-39;
380; Conservative 0; Mismatches 342; Indels
                                                                                                     370 GTATTTACCAAAGATCTTTCGGAATGACAG 399
                                                                                                                             APPLICANT: RADT, Marcus
TITLE OF INVENTION: CERAMIDASE
FILE REPERENCE: P68055USO
CURRENT APPLICATION NUMBER: US/10/182,447
CURRENT FILING DATE: 2002-07-29
PRIOR PLING DATE: 2002-01-27
PRIOR PLING DATE: 2000-01-27
PRIOR PLING DATE: 2000-01-27
PRIOR PLING DATE: 2000-01-27
PRIOR FILING DATE: 2000-01-27
PRIOR FILING DATE: 2000-01-27
PRIOR FILING DATE: 2000-01-37
PRIOR FILING DATE: 2000-01-8
SEQ ID NOS: 14
SEQ ID NOS: 14
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US-10-182-447-4
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Matches 380
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                                                                                                                                CACAGACTTT -- AAAACAIGGCIIGIGICITICCAIACACAICCGGICAGAITIAAAACT 3909
                                                                                                                                                                                                                                          3910 ATTITATAACCACAGGAATTAAACCAAGCAAATAGAGTACTTTCAGATATAAACTGTGTT 3969
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                                                                                                                                                                   CACAGACTITIAAAAAAACATGGGGTGTGTTTTTCCTACACA---AGTCAGATITAAAACT 242
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Sequence 48, Application US/09945527

Sequence 48, Application US/09945527

Sequence 48, Application Wo. US20030055588A1

GENERAL INFORMATION:

APPLICANT: Robison, Keith E.

TITLE OF INVENTION: No. US20030055588A1e1 Nucleic Acid Molecules Encoding

TITLE OF INVENTION: Nucleic Acid and Protein Homologs

FILE REFREENCE: 35800/237985

CURRENT APPLICATION NUMBER: US/09/945,527

NUMBER OF SEQ ID NOS: 65

NUMBER OF SEQ ID NOS: 65

SOFTWARE: FastSEQ for Windows Version 4.0

LENGTH: 744
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                                CCAACAACACATTTTGGCCAGATTGGGATTCTCAATAGATTTTATAGACATTATTCTCC
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Pred. No. 6.8e-85;
0; Mismatches 38; Indels
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Similarity 90.38;
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US-09-945-527-48
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532 AAGTCTTGGGCCAGATTGGGATTCTCAATGGATTTTATAGACATAATTCCCCTGCAAACT 473
                                                                                                                                                                                                                                                                                                                                                                                                                                 234 AAGTGGAGCTTTTGCACTTTATACTTTTTCTGTGAACTATGATAACTATATTTGATATTA 175
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APPLICANT: Mao

APPLICANT: Van (* Veer, Laura Johanna

APPLICANT: Van (* Veer, Laura Johanna

APPLICANT: Van (* Veer, Laura Johanna

APPLICANT: Van (* Veer, Laura Johanna

APPLICANT: Van (* Veer, Laura Johanna

TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients

FILE REPERENCE: 301-168-99

CURRENT APPLICATION NUMBER: 05/298,918

PRIOR PILING DATE: 2003-01-16-18

PRIOR PILING DATE: 2001-06-18

PRIOR APPLICATION NUMBER: 60/380,710

PRIOR FILING DATE: 2002-05-14

PRIOR FILING DATE: 2002-06-14

PRIOR FILING DATE: 2002-06-14

NUMBER OF SEQ ID NOS: 2699
                                                                                                                               3888 ACAICCGGICAGATITAAAACTATITTATAACCACAGGAATTAAACCAAGCAAATAGAGT
                                                                                  472 TAAAAAATAAATAAACCCCTACTTTATAGGACTAATTGTTTGAATTGTATCTTTCTCTGT
                                                                                                                                                                                                                                                    353 GTTTTCAGATATATACCTTGTTTTATACCTTATGTAG-GTGTCCTACATAAGGGTGCCAT
                                                                                                                                                                                                                                                                                                                                 294 GCCCACTGGCTGTGGTAAAATTTAATCCTCATTGCTTTGGGAGTGACTTAAGGCCTTTTG
                                                                                                                                                                                                                    3948 ACTITCAGATATAAACTGTGTTTCATACTTTATGTAGAGTGTGCTATGTATAGGCGGTAT
                                                                                                                                                                                                                                                                                                      GTACCCTGGCTGAAGTAATATTAAC----CATAGCTCTGGGAGGATTTACAGAC----
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Pred. No. 8.5e-27;
0; Mismatches 173; Indels
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; Publication No. US20040058340A1
; GENERAL INFORMATION:
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Mao, Mao
Roberts, Christopher
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Best Local Similarity 62.9%;
Matches 444; Conservative (
                                           3860 TTAAAACA----
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ORGANISM: Homo sapiens
US-10-342-887-2618
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APPLICANT: Linsley, Peter
APPLICANT: Mao, Mao
APPLICANT: Mao, Mao
APPLICANT: Non 't Veer, Laura
APPLICANT: Van de Vijver, Marc
APPLICANT: Van de Vijver, Marc
APPLICANT: Van de Vijver, Marc
APPLICANT: Van de Vijver, Marc
APPLICANT: Van de Vijver, Marc
APPLICANT: Bernards, Rene
TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
FILE REFERENCE: 9301-177-959
CURRENT APPLICATION NUMBER: 60/380,770
PRIOR PILING DATE: 2002-05-14
NUMBER OF SEQ ID NOS: 2699
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PUBLICATION INFORMATION:
DATRAASE ACCESSION NUMBER: Contig56093
DATABASE ENTRY DATE: 2001-06-18
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Publication No. US20030224374A1
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Best Local Similarity 62.9°
Matches 444; Conservative
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3647 ACCTTCTCTGACTCTCTTCTTCCTCAGGTCTGACAACTAATGGTCTCTGGGGA----- 3700
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Best Local Similarity 55.4%;
Matches 201; Conservative C
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US-10-242-535A-50197
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; ORGANISM: Human
US-10-242-535A-50197
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TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptide
FILE REFERENCE: PAOGS-03-27
CURRENT APPLICATION NUMBER: US/10/106,698
CURRENT PILING DATE: 2002-03-27
RRICR APPLICATION NUMBER: US 60/157,137
PRIOR FILING DATE: 1999-09-29
PRIOR FILING DATE: 1999-09-29
PRIOR PRIOR FILING DATE: 1999-11-03
NUMBER OF SEQ ID NOS: 8564
SOFTWARE: Patentin Ver. 3.0
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ORGANISM: Homo sapiens
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LENGTH: 147
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Patent No. US20020155564A1
GENERAL INFORMATION:
APPLICANT: BRADFORD, ERIC
APPLICANT: BRADFORD, ERIC
APPLICANT: HORVAT, SIMON
TITLE OF INVENTION: CLONING OF A HIGH-GROWTH GENE
FILE REFERENCE: 407T-923710US
CURRENT APPLICATION NUMBER: US/09/771,208
CURRENT FILING DATE: 2001-01-26
PRIOR PILING DATE: 1997-12-29
FRIOR FILING DATE: 1997-12-29
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; Sequence 265, Application US/10322281
; Publication No. US20040126762A1
; GENERAL INFORMATION:
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; LOCATION: (1)...(77530)
; OTHER INFORMATION: n = A,T,C or G
US-10-322-281-265
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Best Local Similarity 63.2%;
Matches 115; Conservative (
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SOFTWARE: PatentIn version 3.0
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Publication No. US20040037841A1

GENERAL INFORMATION:

APPLICANT: Liew, C.C.

TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis

TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis

FILE REFERENCE: 4231/2002

CURRENT APPLICATION NUMBER: US/10/085,783A

FRIOR APPLICATION NUMBER: US 60/205,340

PRIOR APPLICATION NUMBER: US 60/275,017

PRIOR APPLICATION NUMBER: US 60/275,017

PRIOR FILING DATE: 2001-03-12

PRIOR FILING DATE: 2001-03-28

NUMBER OF SEQ ID NOS: 58994

SOFTWARE: PatentIn version 3.2

LENGTH: 418
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55.4%; Pred. No. 1.1e-07;
Live 0; Mismatches 140; Indels
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Best Local Similarity 55.44
Matches 201; Conservative
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US-10-085-783A-50197
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; ORGANISM: Human
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267 GCTITCAIAGCCAAGGCITTGCCIAGGGGCTATTAITCCAGCTGGCCAAAGAGA-AGCT 325
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Pred. No. 9.2e-06;
0; Mismatches 64; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: David W. Morris
APPLICANT: David W. Morris
APPLICANT: Marc S. Malandro
TITLE OF INVENTION: NOVel Compositions and Methods in Cancer
FILE REFERENCE: 52945200108.0
CURRENT APPLICATION NUMBER: US/10/322,281
CURRENT FILING DATE: 2002-12-17
NUMBER OF SEQ ID NOS: 866
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 265
LENGTH: 77530
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318008 CTAGGGCTGGTGAGATGGCTCAGCAGTTAAGAGCACTTGCTGGTCTTCCTAAGAACCCAC 317949
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Best Local Similarity 60.9%; Pred. No. 0.00017;
Matches 137; Conservative 0; Mismatches 81; Indels 7;
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JOHER INFORMATION: n is unidentified a, c, g, numer KEY: misc feature incartion: (170625)...(170645)
JOTHER INFORMATION: n is unidentified a, c, g, numer KEY: misc feature is unidentified a, c, g, numer KEY: misc feature is unidentified a, c, g, numer INFORMATION: n is unidentified a, c, g, numer information: n is a, c, g, or t US-09-771-208-20
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OTHER INFORMATION: n is unidentified a, c, g, NAME/KEY: misc.feature
LOCATION: (546998)...(547017)

OTHER INFORMATION: n is unidentified a, c, g, NAME/KEY: misc.feature
LOCATION: (494715)...(494814)

OTHER INFORMATION: n is unidentified a, c, g, CHER INFORMATION: n is unidentified a, c, g,
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                                                     ORGANISM: Mus musculus
FEATURE:
NAME/KEY: misc_feature
LOCATION: (123459)..(123478)
OTHER INFORMATION: n is unidentified a, c,
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LOCATION: (390986)...(391005)
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NAME/KEY: (346860)...(346823)
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LOCATION: (280353)..(280373)
OTHER INFORMATION: n is unidentified a,
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LOCATION: (271829)..(271848)
OTHER INFORMATION: n is unidentified a,
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LOCATION: (317174)..(317193)
OTHER INFORMATION: n is unidentified a,
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SEQ ID NO 20
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                                                                                 Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayakida, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, S., Furuno, M., Hayakida, T., Hirozane, T., Hayakida, S., K. Indo, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Komo, H., Kouda, M., Koya, S., Kurahara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Salto, R., Saltoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Takeda, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Muramatsu, M., and Hayashizaki, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M., and Hayashizaki, Y.

Direct Submission Sibalaki, Y.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue type="urinary bladder"
/clone lib="RIKEN full-length enriched mouse cDNA library"
/dev gtage="adult"
1. .3071
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Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 3071)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 3028.8; DB 3; Length 3071;
Pred. No. 0;
0; Mismatches 2; Indels 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Mus musculus"
/mol type="mrNA"
strain="CS7BL/6J"
/db_xref="FANTOM DB:9530014B21"
/db_xref="taxon:10090"
/clone="9530014B21"
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Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 10.2)
National Institutes of Health, Mammalian Gene Collection (MGC)
National Institutes of Health, Mammalian Gene Collection (MGC)
Upublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. David Rowe
CDNA Library Preparation: Invitrogen Corp
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
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                     TACCCCAGTCACGGGTCAACAGTGTTGTGTTGAGGATCAAACATGGCTCTGTGAAAATAC 3548
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                                                                                            Clone distribution: MGC clone distribution information can be for through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov Series: IRAK Plate: 45 Row: c Column: 7 This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORP
                   X., Hulyk, S.W., Hale, S.M., S., Martin, R.G., Muzny, D.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2829 GGCATTIGGIGCACACGIACATACAGGCAGGCAAAACATTIATACATGIAACGIAAIAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    541 TCTTCTCTCTCTAAGTGCCCTGTGATGCCAAAGCCAGCCCTTCAGAAGTGTTCCTTCTGTC
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                                                                                                                                                                                                                      This clone has the following problem: frame shifted Location/Qualifiers
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/strain="FVB/N-3"
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/tissue type="Mammary tumor. MY
old mouse. Taken by biopsy."
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/note="Vector: pCMV-SPORT6"
            Gunaratne, P.H., Garcia, A.M., Lu,
Yoon, V.S., Kowis, C.R., Lawrence,
Richards, S., Gibbs, R.A.
amg@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.
Matches 1341; Conservative
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/dev stage="embryo." 10.5 dpc"
/lab host="Diper near
/lab host="Diper near
/lab host="Diper near
/lab host="Diper near
/clon=lib="UNIH BMAP Halo." Vector: pYX-Asc; Site 1: EcoR I;
/clon=lib="Organ: Upper Head; Vector: pYX-Asc; Site 1: EcoR I;
Site 2: Not I; The library was constructed according
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarcse
gel.First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with EcoR I adaptor, digested with Not1 and then cloned
directionally into pXX-Asc vector. The library teg
sequence located between the Not I site and the polyA tail
is CGAACTGAAT. This library was created for the University
lowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mental Health (NIMH)."
                                                                                                                                                                                                                                                                                                                                                             CN537424 1717 bp mRNA linear EST 29-APR-2004 UI-M-HSO-cgo-o-10-0-UI.rl NIH_BMAP_HSO Mus musculus cDNA clone IMAGE:30672249 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. James Lin University of Iowa
Tissue Procurement: Dr. James Lin University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
http://genome.uiowa.edu/distribution/mousefl.html
This clone was contributed by the Brain Molecular Anatomy Project
(BMAP)
                                                                                                                                                                    844 GCCAGTCAAGAT-CACGTGATGGCAAGGCAGTGA--CCAGCTTCTCTATT 900
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Best Local Similarity 99.7%; Pred. No. 1e-185;
Matches 715; Conservative 0; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="mana"
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/tissue_type="Upper Head"
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CN537424.1 GI:46865580
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VERSION
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CN537424
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                                                                                                                                                                                   /mol type="mkNA"
//db xref='taxon:10090"
/db xref='taxon:10090"
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the I.M.A.G.E. Consortium/LLNL at:
                       http://image.llnl.gov
Plate: LLAM14067 row: j column: 05
High quality sequence stop: 681.
Location/Qualifiers
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/organism="Mus musculus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Site_1: Sall; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken
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Pred. No. 1.6e-176;
0; Mismatches 3;
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/dev stage="adult"
/lab_host="DH10B"
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/db_xref="taxon:10090"
/clone="9530014B21"
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Best Local Similarity 99.6%;
Matches 683; Conservative
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Contact: Yoshinide Hayashizaki
Laboratorry for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Teurumi-ku, Yokohama, Kanagawa 230-0045, Japan
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                61 GGCCCAGCGAGAAATGGGCTTTTATTGGTGTCCCTTATGTGTCCCTTTCTGTGTGCCCACA
                                                                                                                                                                                                                                                                            181 TATTCGAGTGCGCGCTGGGCTTCGTTTGCTAGCAAAGATGGCTGAGGGGGGTTGAGGAATT
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Gaps .; 0

them based on alignment. FEATURES Location/Qualifiers Location/Qualifiers 1681 / organism="Mus musculus" / mol_type="genomic DNA" / db_xref="taxon:10090" gene <1>61 /locus_tag="HCM1041"	Query Match Best Local Similarity 100.0%; Pred. No. 1.8e-176; Matches 681; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	OY 182 ATGTGCTTGTTCCGCCAGTACGCACGTGCTTCAACAGCGCCATCTACTTAATATGGACG 241	OY 242 CTCCTAGTTGTAGTGGGGATTGGATCTGTCTACTTCCATGCAACGCTGAGTTTCCTGGGT 301	QY 302 CAGAIGCITGARGAACTIGCCAITCIGIGGGITCIGACTITGGCCAIGIGGTIT 361	QY 362 CCCAGGAGGTATTTACCAAAGATCTTTCGGAATGACAGGGCAGGTTCAAGGCAGGTGTG 421	QY 422 TGTGCTGTCTGCAATTACAAGTGCTTGGCGTTTATCAAGCCGGCCATCAACATATT 481 Db 241 TGTGTCCTGTCTGCAATTACAAGTGCTTGGCGTTATCAAGCCGGCATCAACATATT 300	Qy 482 TCCCTGALGATTCTGGGACTTCCATGCACTGCTGCTTGTTGCAGAGGCTGAAGAGGTGT 541 Db 301 TCCCTGATGATTCTGGGACTTCCATGCACTGCTGCTTGTTGCAGAGGTGT 360	Oy 542 GACAATGTGCGTGTTTAAGCTGGGCCTCTTCTCTGGCCTCTGGTGGACTCTGGCTCTC 601 Db 361 GACAATGTGCGTGTTTAAGCTGGGCCTCTTCTCTGGCCTCTGGTGGTGGCTCTGGCTCTC 420	QY 602 TTCTGCTGGACCAAGCCTTCTGAGCTGCTCTCTTTCACTTCCCTAC 661 Db 421 TTCTGCTGGATCAGCGACCAAGCCTTCTGTGCTCCTTTTCACTTCCCTAC 480 QY 652 CTGCACTTGTGTGGCAAATTCTCATCTCTTCTTTCTTTCT
Db 63 CAGTGTTGTGTTGAGGATCAAACATGGCTCTGTGAAAATACTGCCACCCATCTATTGGT 122 Qy 3568 TGGATTTCTCAGGAGTCTGAATCTTCCCTCACGAGTCCTTCTCCCTACCCCTACCCAG 3627 Db 123 TGGATTTCTCAGGAGTCTGATTCTCCCTCAGGAGTCTTCTCTCCCTAACCCTACCCAG 182 Qy 3628 AGCCAACACTGGGATTTGAACCTTCTTGAGTCTTCTTCCTCAGGTCTGACACTAA 3687 Db 183 AGCCAACACTGGGATTTGAACCTTCTTCTTCTTCCTCAGGTCTGACACTAA 3687 Db 183 AGCCAACACTGGGGATTTGAACCTTCTTCTTCTTCTTCCTCAGGTCTGACAACATAA 242 Db 183 AGCCAACACTGGGGATTTGAACCTTCTTCTTCTTCTTCCTCAGGTCTGACAACTAA 242 Dc 183 AGCCAACACTGGGGATTTGAACCTTCTTCTTCTTCTTCTTCTCTCAGGTCTGACAACTAA 242 Dc 183 AGCCAACACTGGGGATTTGAACCTTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT	Qy 3688 FIGETCTCGGGGACACCCAGCTAGGGCCTTCCCCAACTCCTTATCCAGCTGAACTTGGAT 3747 Db 243 TGGTCTCTGGGGACACCCAGCTAGGGCTTCCCCCAACTCCTTATCCAGCTGAACTTGGAT 302	QY 3748 TCTTCCCAACCAGGGTTGACCTGGGTGCTGTTGGTCCCACTGGCCAACACACATCTT 3807 Db 303 TCTTCCCAACCAGGGCTTGACCTGGGTGCTGTTGGTCCCACTGGCCAACACACATCTT 362	OY 3808 GGCCAGATTGGGATTCTCAATAGATTTTATAGACATTATTGTCCCACAGACTTTAAAACA 3867 Db 363 GGCCAGATTGGGGATTGTCAATAGATTTTATAGACATTATTGTCCCACAGAGTTTAAAACA 422	OY 3868 IGGCTIGIGICITICCAIACACAICCGGTCAGAITITAAAACIAITITAIAACCACAGGAA 3927 	OY 3928 TTAAACCAAGGAAATAGAGTACTTTCAGATATAAACTGTGTTTCATACTTTATGTAGAGT 3987	OY 3988 GTGCTATGTATGGCGGTATGTACCCTGGCTGAAGTAATTTAACCATAGCTCTGGGAGG 4047	OY 4048 ATTTACAGACCTTTTGCACTTTTTTTTGTGAACTCTGATAACCATGGTCAATATT 4107	OY 4108 AAAGCCAATAACTGGCATTTCTGTG 4133 	RESULT 6 AY401891 AY401891 BONA linear GSS 12-DEC-2003 BCFINITION BUS MUSCULUS HCM1041 gene, VIRTUAL TRANSCRIPT, partial sequence, ACCESSION AY401891 AY4018

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Sharov, A., Piao, Y., Matcba, R., Dudekula, D.B., Qian, Y., Vanburen, V., Falco, Y., Martin, P.R., Stagg, C.A., Bassey, U.C., Vanburen, V., Falco, G., Martin, P.R., Stagg, C.A., Bassey, U.C., Vanburen, V., Carter, M.G., Hamatani, T., Alba, K., Akutsu, H., Sharova, L., Tanaka, T.S., Kimber, W.L., Yoshikawa, T., Jaradat, S.A., Pantano, S., Nagaraja, R., Boheler, K.R., Taub, D., Hodes, R.J., Longo, D.L., Schlessinger, D., Keller, J., Klunath, T., Hoden, G., Umczawa, A., Vescovi, A.L., Rossant, J., Kunath, T., Hoden, B.L., Curci, A., D'Urso, M., Kelso, J., Hide, W. and Ko, M.S. Transcriptome analysis of mouse stem cells and early embryos PLoS Biol. 1 (3), 410-419 (2003)

Laboratci Dawood B. Dudekula
Laboratciy of Genetics
National Institute on Aging/National Institutes of Health National Institute on Aging/National Institutes of Health
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Wus musculus (house mouse)

Mus musculus

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 670)
   AGGICTGACAACTAATGGICTCTGGGGACACCCAGCTAGGGGCCTTCCCCAACTCCTT-AT
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/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
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Plate: E0830 row: A column: 03
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                                                                                                                     Shultz,M.A., Zhang,L., Gu,Y.-Z., Baker,G.L., Fannuchi,M.V., Padua,A.M., Careke,W.A., Morin,D., Penn,S.G., Jovanovich,S.B., Plopper,C.G. and Buckpitt,A.R. Gene expression analysis in response to lung toxicants: I. Gene expression analysis in response to lung toxicants: I. Sequencing and microarray development and microarray development of Response to Shultz M. Am. J. Respir. Cell Mol. Biol. 30 (3), 296-310 (2004) Contact: Shultz M. Dept. of Molecular Biosciences, School of Veterinary Medicine University of California, Davis

University of California, Davis

1311 Haring Hall, One Shields Avenue, Davis, CA 95616, USA Tel: 530 752 0793

Fax: 530 752 4698

Email: mashultz@ucdavis.edu

Average Phred score is 20 or better. All poor quality data (Phred < 20) and vector/linker sequence stops: 1388.

Location/Qualifiers
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/dev stage="adult"
/dev stage="adult"
/clone lib="Rat lung airway and parenchyma cDNA libraries"
/note="Organ: lung; Vector: pGRM-11Zf(-); Site_1: Eco RI;
Site_2: Not I; mRNA was isolated from microdissected rat
lung airways and parenchyma tissues."
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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16.1%; Score 670.6; DB 6;
Best Local Similarity 87.2%; Pred. No. 1.7e-173;
Matches 854; Conservative 0; Mismatches 104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Rattus norvegicus"
/mol_type="mRNA"
/strain="Sprague-Dawley"
/db_xref="taxon:1016"
/clone="Contig3708"
                                                                                                       (bases 1 to 1388)
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Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)
                                                                                                                AKO85306

Mus musculus 0 day neonate kidney cDNA, RIKEN full-length enriched library, clone:D630008P07 product:similar to CANCER RELATED GENE-LIVER 1 [Mus musculus], full insert sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamanoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Yoneda, X., Ishikawa, T., Ogawa, Y., Izawa, M., Ohara, E., Watchiki, M., Yoneda, Y., Lahikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y., RIKEN integrated sequence analysis (RISA) system--384-format Genome Res. 10 (11), 1757-1771 (2000)
2750 AGACGACCCAGCGACTIGIGAGGCTCATAACCAGCAACTCCAGCCCTGGGGCATCTGACG 2809
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6 (bases 1 to 1173)
Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N.,
                              541 AGACGACCCAGCGACTTGTGAGGCTCATAACCAGCAACTCCAGCCCCGGGGCATCTGACG 600
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Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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                                                                                                                                              RIKEN Genome Exploration Research Group Phase II Team and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Functional annotation of a full-length mouse cDNA collection
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Meth. Enzymol. 303, 19-44 (1999)
99279253
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (house mouse)
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AK085306.1 GI:26:
HTC; CAP trapper.
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                                                                                                                                                                                                                             /notes "Vector: pCMV-SPORT6 (Invitrogen); Site 1: Sall; Site 2: Not1; Mouse cDNA project by the Laboratory of Genetics. National Institute on Aging (NIA), Intramural Research Program, "Inthibitute on Aging (NIA), Intramural This is a long-transcript enriched cDNA library (Ref. Genome Res. 11: 1553-1558 (2001). [PMID: 11544199]). The mRNAs were extracted from a pool of 360 embryos at 4-cell stage. Double-stranded cDNAs were synthesized with an oligo (dT) primer [Invitrogen:
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/dev stage="4-cell"
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Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.

Direct Submission

L. Submitted (16-ARP-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (B-mail:genome-res@gec.riken.jp, Ranagawa 230-0045, Japan (B-mail:genome-res@gec.riken.jp, Pax:81-45-503-9216)

CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.

Division of Experimental Animal Research in Riken contributed to
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/db_xref="G1:26551559"
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similar to CANCER RELATED GENE-LIVER 1 [Mus musculus]
(SPTR|AAL40408, evidence: FASTY, 100%ID, 77.8%length,
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Please visit our web site for further details.
URL:http://genome.gsc.riken.jp/
URL:http://fantom.gsc.riken.jp/.
1.cation/Qualifiers
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Mus musculus (house mouse)
Mus musculus (house mouse)
Mus musculus
Eukaryota, Metazoa; Chordata, Craniata, Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
B 1 (bases 1 to 955)
S Arakawa,T., Carninci,P., Pukuda,S., Furuno,M., Hanagaki,T.,
Hara,A., Hiramoto,K., Hori,F., 1shii,Y., Ito,M., Kawai,J.,
Konno,H., Kouda,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K.,
Ohno,M., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K.,
Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,
Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F.,
Takeda,Y., Tanaka,T., Toya,T., Muramatsu,M. and Hayashizaki,Y.
RIKEN Mouse ESTE (Arakawa,T., et al. 2001) AV227941

AV227941 RIKEN full-length enriched, 14 days embryo liver Mus musgulus cDNA clone 4432411104 3', mRNA sequence. 489 On Nov 1, 1999 this sequence version replaced gi:6180460.
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Fax: 81-45-503-9216 526 609 646 647 GATCAGCGACCAAGCCTTCTGTGAGCTGCTCTCCTTTCACTTCCCCTACCTGCACTG 706 GATCAGCGACCAAGCCTTCTGTGAGCTGCTCCTCCTTTCACTTCCCCTACCTGCACTG 669 Email: genome_resegrac.riken.jp, URL:http://genome.gsc.riken.jp/ Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itch,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. . 10 (10), 1617-1630 (2000)
wagi,K., Pujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Matshiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Re 10 (11), 1757-1771 (2000)

Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara,Y. and Hayashizaki,Y. Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of GCGIGIGITITAAGCTGGGCCTCTTCTCTGGCCTCTGGTGGACTCTGGCTCTCTTCTGCTG GTATTTACCAAAGATCTTTCGGAATGACAGGGGCAGGTTCAAGGCAGTGGTGTCCT GTCTGCAATTACAACGTGCTTGGCGTTTATCAAGCCCGCCATCAACAATATTTCCCTGAT GCGTGTGTTTAAGCTGGGCCTCTTCTCTGGCCTCTGGTGGACTCTGGCTCTTCTGCTG GATTCTGGGACTTCCATGCACTGCGTTGCTTGCAGAGAGCTGAAGAGTGTGAATGT GATTCTGGGACTTCCATGCACTGCGTGCTTGTTGCAGAGCTGAAGAGGTGTGACAATGT

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/dev_stage="5 months"
/dev_stage="5 months"
/dev_stage="5 months"
/dev_stage="5 months"
/clone lib="Nul CGAP Mam2"
/note="Organ: mammary; Vector: pCMV-SPORT6; Site 1: Sal1; Site 2: Not1; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigator providing samples: Gilbert Smith, NIH"
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NHF-WGC http://mgc.nci.nih.gov/.
                                                                                                                       GATTGGGATTCTCAATAGATTTTATAGACATTATTCTCCCACAGACTTTAAAAACATGGCT
                                                                                                   TGTGTCTTTCCATACACATCCGGTCAGATTTAAAACTATTTTATAACCACAGGAATTAAA
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                                       GATTGGGATTCTCAATAGATTTTATAGACATTATTCTCCCCACAGACTTTAAAAACATGGCT
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Plate: LLAM13955 row, g column: 14
High quality sequence stop: 679.
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ilarity 98.7%; Pred. No. 7.5e-169;
Conservative 0; Mismatches 9;
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
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/clone="IMAGE:6437893"
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/strain="FVB/N-3"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Site 1: Sal1; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in
nonredundant cDNA library. Genome Res. . 11 (2), 281–289 (2001)
Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamanaka,I.,
Aizawa,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and
Hayashizaki,Y.
                                                                                                 Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp/) for further details.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /dev_stage="14 days embryo"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                         organism="Mus musculus"
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/clone="4432411104"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tissue_type="liver"
                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                           /mol_type="mRNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                           prepare mouse tissues.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 sex="mixed"
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Best Local Similarity
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5.-ATTCTAGAGGCCGAGGCGGCAAGGGT (30)NN-3. Full-length enriched library was constructed using the Clontech Creator SMART kit and size-selected to contain the 0.5 kb size fraction. Library created in thelaboratory of M. Brownstein (NIMH, NIH). Note: this is a NIH_MGC Library."
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/db xref="taxon:10090"
/clone="IMAGE:6770649"
/lab host="UNGE:6770649"
/clone_lib="NIH_MGC_169"
/note="Organ: Testicles; Vector: pDNR-LIB; Site_1: Sfil (ggccqcttaggcc); Site_2: Sfil (ggccqcttaggcc); GDNA made by oligo-dT priming and directionally cloned. 5' and 3' adaptors were used in cloning as follows:
5'-AAGCAGTGGTATCAACGCAGAGTGGCCATTACGGCCGGG-3' and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GICTGCAATTACAACGTGCTTTGTTATCAAGCCCGCCATCAACAATATTTCCCTGAT 489
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                                                                                               /organism="Mus musculus"
     http://image.llnl.gov
Plate: LLCM308s row: p column:
High quality sequence stop: 536.
Location/Qualifiers
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NIH-MCC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)

L Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Jonathan Kuo, NIMH
CDNA Library Preparation: Michael Brownstein Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
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AGENCOURT 10691314 NIH MGC 169 Mus musculus cDNA clone IMAGES:6770649 5', mRNA sequence.
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617 bp mRNA linear EST 29-APR-2002 UI-M-CGOp-bfj-a-09-0-UI.rl NIH BMAP_Ret4_S2 Mus musculus cDNA clone UI-M-CGOp-bfj-a-09-0-UI 5', mRNA sequence.
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SAGAGAGAGAAGGATCCAAGAGCTCTTTTTTTTTTTTTTVN 3'], cDNA was
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RIKEN. Division of Experimental Animal Research in Riken
Contributed to prepare mouse tissues. 1st strand cDNA was
primed with a primer [5'
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Tel: 81-45-503-9222
Fax: 81-45-503-9216
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and Hayashizaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="urinary bladder"
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/db_xref="taxon:10090"
/clone="9530014B21"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Yoshihide Hayashizaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
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/lab host="MB10B (Life Technologies)"
/clone=lib="NIH BMAP Ret4 52"
/clone=lib="NIH BMAP Ret4 52"
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                                                                                                                                                                                                                                                                                                                                                     CDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa Clone Distribution: Researchers may obtain clones from Research Genetics (www.resgen.com).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             359
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  1 (bases 1 to 617)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
                                                                                                                                                                                                                                Tel: 301 443 9890
Fax: 301 443 9890
Email: mEST@mail.nih.gov
Tissue Procurement: Dr. Xin-Yuan Fu, Yale University School of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1584 GIGACCICTGIGAGAGACAAGGCCTCGITGIAAICGCGGAGGCAGCTCIGGAGGCTTGACT
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Mational Institute of Mental Health
6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
20892-9643, USA
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14.2%; Score 594; DB 5; I
Best Local Similarity 99.5%; Pred. No. 2.1e-152;
Matches 616; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Mus musculus"
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/strain="C57BL/6J"
/db_xref="taxon:10090"
                                                                                Genome Res. 6 (9), 791-806 (1996)
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacren, S., Mahmoud, M., Menen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R. Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AC#11514
1M0184B07R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0184B07 R, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 B., SLC,
84112, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /lab_host="E. Coli strain XLIO-Gold, T1-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus G78L/6J (male) was obtained from the Jackson
TGTAACTCAGGCACCTTCTGCTTTCTGACATTCCATTGTCAGTGGTGAGACTGCACTCAG
                                                                                                                                                 Std Error: 0.00
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Fax: 801 585 7177
Email: ddunnagenetics.utah.edu
Insert Length: 10000 Std Error: 0.
Plate: 0184 row: B column: 07
Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
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/mol_type="genomic DNA"
/strain="C57BL/6J"
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/clone="UUGC1M0184B07"
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Mus musculus
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us-10-017-410-1.rst

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of pWD42 (gi|4732114|gp|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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ORIGIN

1185 7 1066 GTATCCTTTCCAGGCATACGGCTTGCTGGGTTATGTCCATAATGACATCAACAGAGTAG 1125 547 487 TTCTTTGGGAGACCTAGGGCAACCCAAAGTTTCTTGCTGGAGAGAGGTAGCTTGCTGTTTC TICITIGGGAGACCTAGGGCAACCCAAAGTTICTIGCTGGAGAGGGTAGCTTGCTGTTTC 3; Gaps Query Match 13.8%; Score 576.8; DB 8; Length 606; Best Local Similarity 99.2%; Pred. No. 1.2e-147; Matches 601; Conservative 0; Mismatches 2; Indels 3 909 1126 546

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CACCATTICCAGACTCTCAACCCCCTGATAAACAAGACCTTCTGATTTGGTGATGAAAGG 1245 427 CACCATTTCCAGACTCTCAACCCCCTGATAAACAAGACCTTCTGATTTGGTGATGAAAGG

CACGTGTGGGGGTGTGACTAAGACGGGTGGCTTGTCACTCGCACCTCTTAGCTTTCCCCA CACGTGTGGGGGGTGTGACTAAAGACGGGTGGCTTGTCACTCGCACTCTTAGCTTTCCCA 426 1306 366

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.604 GCCICGIIGIAAICGCGGAGGCAGCICIGGAGGCIIGACTGIGGAGCGCCTGIGAAGAIT 1663 GCCTCGTTGTAATCGCGGAGGCAGCTCTGGAGGCTTGACTGTGGAGGC-CTGTGAAGATT 99

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CO744096 Sequence
CO736906 Sequence
CO736906 Sequence
AF347023 Mus muscu
CC605547 Sequence
BX005084 Mouse DNA
BX324222 Mus muscu
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Mus musculus cancer related gene-liver 1 mRNA, complete cds.
AF282864
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AX980438 Sequence
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Graveel, C.R., Jatkoe, T., Madore, S.J., Holt, A.L. and Farnham, P.J.
Expression profilling and identification of novel genes in hepatocellular carcinomas
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Sequence
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Graveel, C.R., Jatkoe, T., Madore, S.J., Holt, A.L. and Farnham, P.J.
Graveel, C.R., Jatkoe, T., Madore, S.J., Holt, A.L. and Farnham, P.J.
Graveel, C.R., Jatkoe, T., Madore, S.J., Holt, A.L. and Farnham, P.J.
Garcinomas using oligonucleotide microarrays and representational difference analysis
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Submitted (27-JUN-2000) Oncology, University of Wisconsin, 1400
                                                         AF323976 | AX206797 | AF347024 |
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Farnham, P.J. and Graveel, C.R.
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Location/Qualifiers
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Sequence 6 from Patent WO0155408.
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/note="cloning
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Kazusa-Kamatari, Kisarazu, Chiba 292-0818, Japan
(E-mall:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
MEDO human CDNA sequencing project supported by Ministry of
Economy, Trade and Industry of Japan; CDNA hil insert sequencing:
Research Association for Biotechnology (RAB); CDNA library
construction: Helix Research Institute (HRI) (supported by Japan
Key Technology Center etc.); 5- & 3'-end one pass sequencing: RAB,
HRI, and Biotechnology Center, National Institute of Technology and
Evaluation; clone selection for full insert sequencing: HRI and
RAB, annotation: HRI and RAB.
Location/Qualifiers
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Sugiyana,T., Irie,K., Otsuki,T., Sato,H., Wakamatsu,A., Ishii,S.,
Xamamoto,J., Isono,Y., Kawai-Hio,Y., Saito,K., Nishikawa,T.,
Ximura,K., Yamashita,H., Matsuo,K., Nakamura,Y., Sekine,M.,
Kikuchi,H., Kanda,K., Wagatsuma,M., Murakawa,K., Kanehori,K.,
Takahashi-Fujii,A., Oshima,A., Sugiyama,A., Kawakami,B., Suzuki,Y.,
Sugano,S., Nagahari,K., Masuho,Y., Nagai,K. and Isogai,T.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                           LeuLeuValAlaGluLeuLysArgCysAspAsnValArgValPheLysLeuGlyLeuPhe
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Homo sapiens cDNA FLJ41587 fis, clone CTONG2020638.
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oligo capping; fis (full insert sequence)
Homo sapiens (human)
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Isogai,T. and Yamamoto,J.
Direct Submission
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Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see http://genome.wustl.edu/gsc
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                                                                                                                             Patent: WO 0155408-A 6 02-AUG-2001;
Memorec Medical Molecular Research Cologne Stoffel GmbH (DE)
Location/Qualifiers
                                                               Craniata; Vertebrata; Eutele
Catarrhini; Hominidae; Homo.
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Conservative:
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Mammalia; Eutheria; Primates;
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Hofmann, K. and Conradt, M.
            GI:15394643
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linear PRI 09-JAN-2002
2, complete sequence.
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Direct Submission
Submitted (09-DBC-1999) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
4 (bases 1 to 149462)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  USA
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                                                                                                                                  GinGlyProValileArgPheTrpProSerGluLysTrpAlaPheIleGlyValProTyr 260
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all regions were double stranded, sequenced with an alternate
chemistry, or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats, all regions were covered by sequence
from more than one subclone; and the assembly was confirmed by
                                                                                                                                                                                                  CAAGGCCCTGTCATCAAATTCTGGCCCAGCGAGAAATGGGCCCTTCATTGGTGTCCCCTAT 777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 149462)
Suleton,J.B. and Waterston,R.
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Submitted (09-JAN-2002) Department of Genetics, Washington
Submitted (09-JAN-2002) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108,
On Jan 9, 2002 this sequence version replaced gi:14165368.
AlaSerTyrLeuGlyCysValCysPheAlaTyrPheAspAlaAlaSerGluIleProGlu
                                   GCTGCCTACCTGGGCTGTGTATGCTTTGCCTACTTTGATGCTGCCTCAGAGATTCCTGAG
                                                                                                                                                                                                                                                                         275
                                                                                                                                                                                                                                                                                                        The sequence of Homo sapiens BAC clone RP11-470J24
Unpublished (2001)
3 (bases 1 to 149462)
                                                                                                                                                                                                                                                              ValSerLeuLeuCysAlaHisLysLysSerProValLysIleThr
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Contact: sapiens@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA
from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Toward a complete human genome sequence Genome Res. 8 (11), 1097-1108 (1998)
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Homo sapiens BAC clone RP11-470J24
AC017081
AC017081.8 GI:18093316
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Length:
Matches:
Conservative:
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2592. .12706
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           The RPCI-11 human BAC library was made from the blood of one male donor, as described by Oscegawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at the Roswell Park Cancer Institute
(http://bacpac.med.buffalo.edu)
                                                                                                                                                                          The clone sequenced to the left is RP11-310K15, 2000 bp overlap; the clone sequenced to the right is RP11-156A1, 2000 bp overlap. Actual start of this clone is at base position 190775 of RP11-310K15; actual end is at base position 28935 of RP11-156A1.
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hote="match to EST AW614820 (NID:g7320006) hg80c08.xl"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note="match to EST AA056210 (NID:g1548612) zf62g06.81"
                                                                                                                                                                                                                                                       The sequence between 81601 and 81703 is covered only by a pcr product of clone DNA. Unresolved tandem repeat regions exist between 81548 and 83183, 126196 and 127426.

Location/Qualifiers
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Mammalia, Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buttow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McKwan, P.J.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Luu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
L. Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.B. Consortium/LINL at: http://image.llnl.gov Series: IRAK Plate: 132 Row: o Column: 4 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 21314857.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield, Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin, Letticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline Schein, Dannes Smailus, Michael Smith, Lorraine Spence, Jeff Stott, Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy, George Yang, Scott Zuyderduyn, Marco Marra.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (07-OCT-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbbs-r@mail.nih.gov
Tissue Procurement: Dr. James Lin, University of Iowa
CDNA Library Preparation: M. Bento Soares, University of Iowa
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
info@bcgsc.bc.ca
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/product="CRG-L1 protein"
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
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Mus musculus cancer related gene-liver 1, mRNA (cDNA clone
MGC:69583 IMAGE:6839525), complete cds.
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                                                                                                                                                                                                                                                                                                                                                 Submitted (04-OCT-2002) Nori Satoh, Kyoto University, Department
Zoology; Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
(E-mail:satoh@ascidian.zool.kyoto-u.ac.jp, Tel:81-75-753-4095,
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                                                                                                                                                                                                        Satou,Y., Yamada,L., Mochizuki,Y., Takatori,N., Kawashima,T. Sasaki,A., Hamaguchi,M., Awazu,S., Yagi,K., Sasakura,Y., Nakayama,A., Ishikawa,H., Inaba,K. and Satoh,N. A cDNA resource from the basal chordate Ciona intestinalis Genesis 33 (4), 153-154 (2002)
                                                                                                                                                                                                                                                                                                                                                                                       Fast 175-705-1113)
Ciona intestinalis CDNA Project (URL:
http://ghost.zool.kyoto-u.ac.jp/indexr1.html).
ce | Location/Qualifiers |
location/Qualifiers |
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                                                                   1429 bp mRNA clone:citb013n14,
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Gaps:
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Satou, Y. and Satoh, N. Direct Submission
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/protein_id="AAH59819.1"
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db_xref="G1:375905.20"
db_xref="Locusid:3103.79"
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FPYLHGVWHTLICLASYLGCVCFAYFDAASEIPEQGPVIRFWPSEKWAFIGVPYVSLL
CAHKKSPVKIT"
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                                                                                                                                                      4078
229
0
0
46
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Matches:
Conservative:
Mismatches:
Indels:
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83.27%
82.80%
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Best Local Similarity:
Query Match:
DB:
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NTFSNFLFILLPPVLIMLFKEYGRFVTPGIHVIWVLLIVVGLSSMYFHATLSLIGQLL
DELAILWVFWAAFGLFYPKRYYPKFWKNDRKTFSWLMLLSAIAATGLSWWKPIVNAFV
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/note="alignment with genomic scaffold AE003665. gene does
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      87 PheLeuGlyGlnMetLeuAspGluLeuAlaIleLeuTrpValLeuMetCysAlaLeuAla 106
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125
54
77
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                                                                             organism="Drosophila melanogaster"
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Conservative:
Mismatches:
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          cdna@fruitfly.berkeley.edu
                                                                                                                                                                             /map="38B4-38B5"
                                                                                                                                                                                                                                                                                                                                                                                             /codon_start=1
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Submitted (18-DEC-2001) Berkeley Drosophila Genome Project,
Lawrence Berkeley National Laboratory, One Cyclotron Road,
Berkeley, CA 94720, USA
Sequence submitted by:
Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory
Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory
Berkeley, CA 94720
This clone was sequenced as part of a high-throughput process to
sequence clones from Drosophila Gene Collection | (Rubin et al.,
Science 2000). The sequence has been subjected to integrity checks
within 100 kb in the genome. Thus we believe the sequence to
reflect accurately this particular cDNA clones that may
within 100 kb in the genome. Thus we believe the sequence to
reflect accurately this particular cDNA clones that may
have not been detected in our initial analyses such as internal
priming, priming from contaminating genomic DNA, retained introns
due to reverse transcription of unspliced precursor RNAs, and
reverse transcriptase errors that result in single base changes.
For further information about this sequence, including its location
and relationship to other sequences, please visit our Web site
(http://fruitfly.berkeley.edu) or send email to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INV 20-DEC-2001
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Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta; Pterygota;
Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta; Pterygota;
Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroides, Drosophila, Brachycera, Muscomorpha,
I (bases 1 to 2318)
Stapleton, M., Brokstein, P., Hong, L., Agbayani, A., Carlson, J.,
Champe, M., Chavez, C., Dorsett, V., Dresnek, D., Farfan, D., Frise, E.,
George, R., Gonzalez, M., Guarin, H., Kronmiller, B., Li, P., Liao, G.,
Patel, S., Phouanenavong, S., Wan, K., Yu, C., Lewis, S.E., Rubin, G.M.
AlaValValCysValLeuSerAlaIleThrThrCysLeuAlaPheIleLysProAlaIle 146
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                                                                                                                                                                                                                                                                                                                  745
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                                                                                                                                                                                            LysArgCysAspAsnValArgValPheLysLeuGlyLeuPheSerGlyLeuTrpTrpThr 186
                                                                                                                                                                                                                                                                                        LeuAlaLeuPheCysTrpIleSerAspGlnAlaPheCysGluLeuLeuSerSerPheHis 206
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AY071232.1 GI:17945605
FLI_CDNA.
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ACCESSION
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KEYWORDS
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PAT 30-AUG-2001
            303 TCATCCAACATCGCCGAGTTCGTGAACACGTTTAGCAACTTCCTGTTCATCCTACTGCCG 362
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                                                  ProlleCysMetCysLeuPheArgGlnTyrAlaThrCysPheAsnSerGlyIleTyrLeu 66
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      87 PheLeuGlyGlnMetLeuAspGluLeuAlaIleLeuTrpValLeuMetCysAlaLeuAla
                                                                                                                                                                                                                                                                  127 AlavalvalCysvalLeuSerAlaIleThrThrCysLeuAlaPheIleLysProAlaIle
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27 ValProAlaIleAlaGluPheTyrAsnThrIleSerAsnValLeuPhePheIleLeuPro
                                                                   67 IleTrpThrLeuLeuValValValGlyIleGlySerValTyrPheHisAlaThrLeuSer
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Patent: WO 0155408-A 4 02-AUG-2001;
Memorec Medical Molecular Research Cologne Stoffel
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/db_xref="taxon:9606"
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AX206797
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NTFSNFLFILLPPVLIMLFKEYGRFVTPGIHVIWVLLIVVGLSSMYFHATLSLIGQLL
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YLHGFWHIFIFIAAYTVLVLFAXFYVESELPQRQPLLKYWPKNEFEFGIPFISIRNPG
KALRNTI"
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CAGAGAGITAGIGACCAGAGGGICTACCGCCTGGGCAICCGATCGACGACCGICTGGGCT
                          LeuAlaLeuPheCysTrpIleSerAspGlnAlaPheCysGluLeuLeuSerSerPheHis
                                                                               PheProTyrLeuHisCysValTrpHisIleLeuIleCysLeuAlaSerTyrLeuGlyCys
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|mol_type="mRNA"
| db_xref="taxon:7227"
|chromosome="2"
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|gene="bwa"
|note="ceramidase; BWA"
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 795)
Mao,C., Xu,R. and Obeid,L.M.

Homo sapiens (human)

Homo sapiens

AUTHORS REFERENCE

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YGWVTWALVDANYEMPGGFTLKVRYWPRDSWFVGLPYVEIRGDDKDC"
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                                                                                                                                   South
                                                                               Mao,C., Xu,R. and Obeid,L.M.
Direct Submission
Submitted (08-FEB-2001) Medicine, Medical University of Carolina, 171 Ashley Avenue, Charleston, SC 29425, USA
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/function="deacylates ceramide

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/db_xref="taxon:9606"
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Sequence 22840 from Patent W002068579.
CQ736906.1 GI:42333767
                                                CQ736905 315 bp DNA Sequence 22839 from Patent WO02068579. CQ736905
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Mao,C., Xu,R., Szulc,Z.M., Bielawski,J., Becker,K.P., Bielawska,A., Galadaris,A.H., Hu, W. and Obeid,L.M.
Cloning and Characterization of a Mouse Endoplasmic Reticulum Alkaline Ceramidase: AN ENZYME THAT PREFERENTIALLY REGULATES METABOLISM OF VERY LONG CHAIN CERAMIDES
12783875
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Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W.
Kits, such as nucleic acid arrays, comprising a majority of
humanexons or transcripts, for detecting expression and other uses
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Patent: WO 02068579-A 22840 06-SEP-2002;
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/db_xref="taxon:9606"
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a fatty acid"
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                                    South
Direct Submission
Submitted (08-FEB-2001) Medicine, Medical University of
Carolina, 171 Abhley Avenue, Charleston, SC 29425, USA
Location/Qualifiers
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Conservative:
Mismatches:
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Search completed: November 21, 2004, 08:54:39 Job time : 3506 secs

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score:

Title: Perfect

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Run on:

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Aak52550 Human fol
Ab124043 Drosophil
Ab124042 Drosophil
Ab120432 Drosophil
Ab10432 Drosophil
Ab48640 Human cer
Ab211993 Human pol
Adm4511 Novel hum
Aa96499 CDNA enco
Aac40178 Arabidops
Adc87616 Human GPC
Ab115072 Human GPC
Ab115072 Human pro
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Abv22202 Human pro
Abv22064 Human pro
Ab190053 Human pol
Aaf13013 Aspergill
Aaf13013 Aspergill
Aah07955 Human cDN
Abac8192 Human GPC
Aac8192 Human GPC
Ab123205 Prosophil
Ab123205 Prosophil
Ab123205 Prosophil
Ad687290 Human GPC
Aa880960 DNA encod
Aas66068 DNA encod
Aad68280 Human tum
Aad68280 Human tum
Adio6642 Human 3T3
Adi21948 Novel hum
Adi21468 Novel hum
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Adc87292 Human GPC
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Adc86916 Human GPC
                                                Aak51566 Human pol
Aak52550 Human pol
Aah48639 Human cer
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/product= "Liver tumour marker protein, CRG-L1"
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ADC87616
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ADC87290
AAS80960
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ADC87192
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ABL24043
ABL24043
ABL30432
AAH48640
ABZ11993
ADM44511
AAA96499
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                                                                                                                   November 20, 2004, 21:28:52; Search time 433 Seconds
                     GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                   nucleic search, using frame plus p2n model
                                                                                                                                                                                                                                                                                                                                                                           hits satisfying chosen parameters:
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                                                                                                                                                                                                  The invention relates to a polypeptide designated as CRG-LIJ), which is differentially expressed in liver tumours relative to normal expression in normal liver tissues, designated CRG-LiJ. Also included are the encoding polynucleotides (in the case of the human sequence, mapping to chromosome 9p), expression constructs, host cells, anti-CRG-LiJ sequence in the diagnostis of hepatocellular cancer in tumour cells from liver of a human or non-human animal. The CRG-LiJ protein and polynucleotide are useful as diagnostic markers for a liver cancer in humans animals, and as a system for assessing putative
                                                                                                 Novel polypeptide designated as CRG-L1, useful as diagnostic marker for liver cancer, is differentially expressed in liver tumors relative to normal liver tissues.
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                                                                                                                                                                                                                                                                                                                                                                            therapeutic agents. The present sequence encodes mouse CRG-L1
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Mismatches:
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The present invention describes a method for detecting a bladder cancerassociated transcript in a cell from a patient. The method comprises contacting a blological sample from the patient with a polymucleotide that selectively hybridises to a sequence that is 80 % identical to a table of sequences (see ACC50951 to ACC51059). ACC50951 to ACC51059 encode the human bladder cancer-associated proteins given in ABR48146 to ABR48242). Bladder cancer-associated proteins given in ABR48146 to ABR48242). Bladder cancer-associated sequences from the present invention have cytostatic activities, and can be used in antisense gene therapy and in vaccine production. The method can be used for detecting a bladder cancer-associated transcript in a cell from a patient. The method is useful in diagnosing or treating bladder cancer and in screening for compounds that modulate bladder cancer, such as hormones or antibodies. The nucleic acid molecules from the present invention may be used in various screening and diagnostic methods, and for gene therapy, vaccine and/or antisense/inhibition applications
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08-NOV-2001; 2001US-0343705P.
13-NOV-2001; 2001US-035666FP.
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Human; differential expression; cancer; angiogenic disorder; fibrotic disorder; psoriasis; isofanemia; heart disease; atherosclerosis; inflammatory disease; autoimmune disease; retinal neovascularistaion syndrome; scarring; uterine fibroid; defection; diagnosis; prognosis; drug screening; drug targeting; wound healing; contraception; cytostatic; cardiant; immunomodulatory; vulnerary; gene therapy; vaccine; gene; ss.
                                                                                                         Cancer/angiogenesis/fibrosis-related nucleic acid, SEQ ID NO:151.
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21-NOV-2001; 2001US-0332464P.
29-NOV-2001; 2001US-0334339P.
03-DEC-2001; 2001US-0345394P.
14-DEC-2001; 2001US-0346376P.
08-JAN-2002; 2002US-0347349P.
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2002US-0356714P.
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04-APR-2002, 2002US-0370110P.
12-APR-2002, 2002US-037246P.
05-JUN-2002, 2002US-0386614P.
16-JUL-2002, 2002US-0396839P.
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13-FEB-2002;
20-FEB-2002;
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22-JUL-2002;
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ADN38833;
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Hevezi PA; Gish KC, Glynne R, Her Wilson KE, Zlotnik A; Aziz N, Ginsburg WM, Murray R, Watson SR, WPI; 2003-468649/44. Aziz N. Afar D, i Mack DH,

P-PSDB; ADN38834

Determining the presence or absence of a pathological cell in a patient, useful for diagnosing, prognosing or treating cancer, comprises detecting a nucleic acid in a biological sample.

Claim 8; SEQ ID NO 151; 1385pp; English

The invention relates to nucleic acids and proteins (ADN38683-ADN40064)

Concers or whose expression is upregulated or downregulated in specific cancers or other diseases such as angiogenic or fibrotic disorders, and to methods of determining the presence or absence of a pathological cell in a patient by detecting a nucleic acid at least 80% identical to those of the invention or by detecting a polypeptide of the invention. The invention also relates to expression vectors and host cells comprising a nucleic acid of the invention, antibodies which specifically bind a polypeptide of the invention; use of such antibodies for drug targeting; and methods of screening for modulators of activity or expression of the polypeptides and nucleic acids. The nucleic acids, polypeptides, and methods are useful for diagnosing, prognosing and treating cancer and other conditions such as psoriasis, ischaemia, heart disease, atherosclerosis, inflammatory diseases, autoimmune diseases, retinal neovascularistation syndromes, scarring and uterine fibroids. They may also be useful in wound healing and in contraception. The present sequence represents a nucleic acid sequence of the invention.

ADN38833 standard; cDNA; 4212 BP

ADN38833 ID ADN3 RESULT 3

(first entry)

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Human cDNA encoding a liver tumour marker protein, CRG-L1.
          25-NOV-2002
                                                                      Homo sapiens
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                                                                                                     MetGlyAlaProHisTrpTrpAspHisLeuArgAlaGlySerSerGluValAspTrpCys
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                                                                                                                                       21 GluAspAsnTyrThrIleValProAlaIleAlaGluPheTyrAsnThrIleSerAsnVal
 Other;
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Conservative:
Mismatches:
Indels:
 932 G; 1339
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Sequence 4212 BP; 1047 A; 894
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ABS54149 standard; cDNA; 828

ABS54149

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to a polypeptide designated as CRG-LL), which is differentially expressed in liver tumours relative to normal expression in normal liver tissues, designated CRG-LL. Also included are the encoding polynucleotides (in the case, for the human sequence, mapping to chromosome 9p), expression constructs, host cells, anti-CRG-LL antibodies, identifying modulators of CRG-LL, and the use of the CRG-LL antibodies in the diagnosis of hepatocellular cancer in tumour cells from liver of a human or non-human animal. The CRG-LL protein and polynucleotide are useful as diagnostic markers for a liver cancer in humans and non-human animals, and as a system for assessing putative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel polypeptide designated as CRG-L1, useful as diagnostic marker for liver cancer, is differentially expressed in liver tumors relative to normal liver tissues.

        1 MetGlyAlaProHisTrpTrpAspHisLeuArgAlaGlySerSerGluValAspTrpCys

        1 MetGlyAlaProHisTrpTrpAspHisLeuArgAlaGlySerSerGluValAspTrpCys

        2 ATGGGCCCCCGCACTGGTGGAGCTGCAGGCTGGTAGCTCGGAGGTGGACTGGTGC

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                                                                                                                                                                                                                                     "Liver tumour marker protein, CRG-L1"
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Human; ss; gene; liver cancer; liver tumour; CRG-Ll;
hepatocellular cancer; chromosome 9p.
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91.27*
92.86*
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Best Local Similarity:
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|AACAGTGACATCTACTTAATCTGGACTCTTTTGGTTGTAGTGGGAATTGGATCCGTCTAC
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/note= "No stop codon given"
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This invention describes novel human ceramidase (I) containing a specific attructural motif which has antiproliferative, anticancer, anti-eczema, antipsoriasis and dermatchological activity. (I) cleave ceramide, resulting in formation of sphingosine. (I), or the nucleic acid (II) encoding it, are used for diagnosis, prevention or treatment of diseases associated with ceramide defects, particularly altered cell proliferation (cancer) or altered ceramide layers on the skin (neurodermatitis, eczema, psoriasis), also for targeted modification of the permeability barrier by ceramidase or its activators, e.g. for transcutaneous delivery of substances. Specifically they are used for diagnosis of ichthyosis, particularly lamellar ichthyosis ICR2. (I) can also be used in cosmetics. This sequence encodes human ceramidase X3
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                                                                                                                                          New ceramidase containing specific structural motif, useful for diagnosis, prevention and treatment of ceramidase defects, e.g. ichthyosis, also in cosmetics.
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Query Match: 73.45% Indels: 116 DB: 2	-10-017-410-2 (1-275) x ADL06640 (1-1527) 37 IleSerAsnValLeuPhePheIleLeuProProlleCysMetCysLeuPheArgGlnTyr 56	DB 1/9 AICAGCAATGICTIATITITICATCICCCCATCIGCATGIGGITGGICAGIA 238 Qy 57 AlaThrCysPheAsnSerGlyIleTyrLeuIleTrpThrLeuLeuValValValGlyIle 76 Db 239 GRAACATGATGATGATAATTAATTAATTAATTAATTAATTAA	7 GlySerValTyrPheHisAlaThrLeuSerPheLeuGlyGlnMetLeuAspGluLeuAla 96	97 IleLeuTrpValLeuMetCygAlaLeuAlaMetTrpPheProArgArgTyrLeuProLys 11	Db 359 GTCCTTTGGGTTCTGATGTGTGTCTTGGCCATGTGGTTCCCCAGAAGGTATCTACCAAAG 418 Oy 117 IlePheArgAsnAspArgGTyArgPheLysAlaValValCysValLeuSerAlaIleThr 136 Db 110	137 ThrCysLeuAlaPhelleLysProAlaileAsnAsnileSerLeuMetileLeuGlyLeu	DD 4/9 ACGTGCCTGGCATTTGTCAAGCCTGCCATCAACATCTCTCTGATGACCCTGGGGAGTT 538 Qy 157 ProcysThrAlaLeuLeuValAlaGluLeuLys	Db 539 CCTTGCACTGCACTGCTCATCGCAGAGCTAAAGAGGCATGAGAGGAACCAGCGAAGGAGA 598	Oy 167167 167 167	168ArdCvaAsbAshValArdValPheLvsLeuClvLeuPheSerGlvLeuPheSerGlvLeuTr				Db 779 CTTCAACTTCCCCTACCTGCACTGGGGGGGGGGGTCAGATGGTTCAGAAGCCACTG 838	OY 214 214 Db 839 AAAGCACACTITGTAAAAAGCIGAATIGACICCAGGGAGCAGCTIAGCCGGAACGAAAG 898	Qy 214 214	899 GCCTGATTGTCATGCTTAGCAGGACTATTTAAGAACATTCTAAAACGGGTCCCCAAATTGC 95	Db 959 TGAAGATTTATCATCCTGCTATTCCAGGGATTGTTGTTGTTAGTCTTCCTTTCCTATTA 1018	Oy 215	223 TyrLeuGlyCysValCysPheAlaTyrPheAspAlaAlaSerGluIleProGluGlnGly 242	DD 10/9 TACCTGGGCTGTGTATGCTTACCTACTTTGATGCTGCCTCAGAGATTCCTGAGCAGGGC 1138 Qy 243 ProVall1eArgPheTrpProSerGluLySTrpAlaPheIleGlyValProTyrValSer 262
Cy 161 LeuLeuValAlaGluLeuLysArgCysAspAsnValArgValPheLysLeuGlyLeuPhe 180 A 2	181 SerGlyLeuTrpTrpThrLeuAlaLeuPheCysTrpIleSerAspGlnalaPheCysGlu 20	Qy 201 LeuLeuSerSerPheHisPheProTyrLeuHisCysValTrpHisIleLeuIleCysLeu 220	Oy 221 AlaSerTyrLeuGlyCysValCysPheAlaTyrPheAspAlaAlaSerGluIdeProGlu 240 :::	Qy 241 GlnGlyProValIleArgPheTrpProSerGluLysTrpAlaPheileGlyValProTyr 260	Oy 261 ValSerLeuLeuCysAlaHisLysEveProValLysIleThr 275	RESULT 6 ADLO6640 ID ADLO6640 standard; cDNA; 1527 BP.	ADL06640;	DI 05-MAY-2004 (Ilrst entry) XX DE Human 3T3 cell conversion promoter PP11646 cDNA.	XX XW 3T3 cell conversion; promoter; human; gene; Bs. XX		EN CN1403477-A. XX PD 19-MAR-2003	12	12-SEP-2001; 2001CN-00126725.	PA (SHAN-) SHANGHAI XINSHIJIB GENB TECHN DEV CO LTD. XX PI Gu J, Yang S;	XX DR WPI; 2003-494226/47. DR P-PSDB; ADL06641.	AA PT Human protein with function of promoting 3T3 cell conversion and its PT coding sequence.		This invention describes a novel human protein with 3T3 cell promoting function, polynucleotides encoding the polypeptide	C also discloses to producing the polypeptide. The present invention CC also discloses the agonist resisting the polypeptide and its treatment CC effect. The present invention also discloses the application of the CC polynucleotides encoding the human protein with 313 cell conversion	promoting function. Sequence 1527 BP; 376 A; 357 C; 383 G; 411 T; 0 U; 0 Other;	Alignment Scores: 3.05e-102 Length: 1527 Pred. No.: 3.05e-102 Length: 22 Score: 1110.50 Matches: 22 Bercent Similarity: 66.20# Conservative: 13 Paget Incal Similarity: 67.44# Mignative: 4

1527 222 13

Length:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATCAGCAATGTCTTATTTTTCATTTTACCGCCCATCTGCATGTGCTTGTTTCGTCAGTAT 238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This invention describes a novel human protein with 3T3 cell conversion promoting function, polynucleotides encoding the polypeptide and the recombinant process of producing the polypeptide. The present invention also discloses the agonist resisting the polypeptide and its treatment effect. The present invention also discloses the application of the polynucleotides encoding the human protein with 3T3 cell conversion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GlySerValTyrPheHisAlaThrLeuSerPheLeuGlyGlnMetLeuAspGluLeuAla
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                its
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 LeuLeuCysAlaHisLysLysSerProValLysIleThr 275
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Matches:
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                                                                                                                                                                                                         conversion; promoter; human; gene;
                                                                                                                                                                            Human 3T3 cell conversion promoter PP11646
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1110.50
66.20%
62.54%
73.45%
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                                                                                        standard; DNA; 1527
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61 AsnSerGlyIleTyrLeuIleTrpThrLeuLeuValValGlyIleGlySerValTyr 80
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13-SEP-2002; 2002US-00323739.
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                                                                                                                                                                                                                                                                                                                                                New polynucleotides and secreted proteins, useful for treating myeloid or lymphoid cell disorders, in bone cartilage, tendon, ligament and nerve tissue growth or regeneration, in wound healing, and in tissue repair and
            bone cartilage tissue growth; tendon tissue growth;
ligament tissue growth; nerve tissue growth; regeneration; wound healing;
tissue repair; tissue replacement; burn; incision; ulcer; cancer; human;
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                                                                                                                                                                                                                                                         Wang J;
Wang D;
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                                                                                                                                                                                                                                                       RW, Ren F, Zhang J, Zhao QA, Wang
Weng G, Zhou P, Drmanac RT, Wang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1623 BP; 305 A; 457 C; 382 G; 479 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length:
Matches:
Conservative:
Mismatches:
myeloid cell disorder; lymphoid cell disorder;
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Ghosh M, Xue AJ, Wehrman T,
Haley-Vicente D;
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1087.00
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13-SEP-2002; 2002US-00323739
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                                                                                                                                                                                                                           (HYSE-) HYSEQ INC
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Best Local Similarity:
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                                                                                                       WO2003025148-A2
                                                                              Homo sapiens
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(first entry)

06-NOV-2001

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The invention relates to an isolated polynucleotide encoding a polypeptide with biological activity. The polynucleotides and polypeptides are useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders and other traits, to assess biodiversity, as nutritional sources or supplements. The polynucleotides may also be used as molecular weight markers, chromosome markers or map related gene positions, or as an antigen to raise anti-DNA antibodies or elicit immune response. The polypeptides are useful for raising antibodies, as markers for rissues in which the corresponding polypeptide is expressed, for re-engineering damaged or diseased tissues, for treating myeloid or lymphoid cell disorders, in cone cartilage, tendon, ligament and/or nerve tissue growth or regeneration, in wound healing in tissue repair and replacement, in healing of burns, incisions and ulcers, and in treating cancer. The present sequence represents a novel human expressed sequence tag, EST.
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                Wang J;
Wang D;
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                Zhang J, Zhao QA,
ou P, Drmanac RT,
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Matches:
Conservative:
Mismatches:
Indels:
Lang XT, Asundi V, Goodrich RW, Ren F, Zhang
Ghosh M, Xue AJ, Wehrman T, Weng G, Zhou P,
Haley-Vicente D;
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Best Local Similarity:
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CTGATGTGTTTAGCCATGTGGTTC 485

AAK51566 standard; cDNA; 1215

RESULT 10

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AAK51566

AAK51566 ID AAKS XX AC AAK5 XX

LeuMetCysAlaLeuAlaMetTrpPhe 109

101

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production of other cytokines in other cell populations. The production of other cytokines in other cell populations. The polymucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activity, inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation. Note: Records for SEQ ID NO 2110 (AAX52581), 2111 (AAX52582) and 3666 (AAM80020) are omitted as the relevant pages from the sequence listing were missing at the time of publication
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleic acids encoding polypeptides with cytokine-like activities, useful in diagnosis and gene therapy.
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Conservative:
Mismatches:
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                                                            Human polynucleotide SEQ ID NO 111.
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Ma Y, Zhao QA, Wang D, Wang
Xue AJ, Yang Y, Wejhrman T,
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20-JUN-2000; 2000US-00598075.
19-JUL-2000; 2000US-00620325.
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15-SEP-2000; 2000US-00653561.
20-OCT-2000; 2000US-00693325.
30-NOV-2000; 2000US-00728422.
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uleualalieleuTrpValleuMetCysAlaLeuAlaMetTrpPheProArgArgTyrLe 114
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             uProfysIlePheArgAsnAspArgGlyArgPheLysAlaValValCysValLeuSerAl 134
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rAsnThrIleSerAsnValLeuPhePheIleLeuProProIleCysMetCysLeuPheAr
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                                                                               74 lGlylleGlySerValTyrPheHisAlaThrLeuSerPheLeuGlyGlnMetLeuAspGl
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Nucleic acids encoding polypeptides with cytokine-like activities, useful

Claim 1; Page 4462; 6221pp; English.

diagnosis and gene therapy

2001-476283/51.

WPI; 2001-476283/: P-PSDB; AAM79417.

ZW;

Wang

LC, Cao Y; Chen R, War

χα C,

Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xi Ma Y, Zhao QA, Wang D, Wang J, Zhang J, Ren F, Xue AJ, Yang Y, Wejhrman T, Goodrich R;

03-FEB-2000; 2000US-00496914. 27-ARP-2000; 2000US-00560B75. 20-UTN-2000; 2000US-00598075. 19-UTL-2000; 2000US-00620325. 01-SEP-2000; 2000US-00654936. 15-SEP-2000; 2000US-00654936.

2000US-00728422

(HYSE-) HYSEQ INC

05-FEB-2001; 2001WO-US004098

WO200157190-A2

09-AUG-2001

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The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to cytokine, call proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activity, inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leuksemia, nervous system disorders, arthritis and inflammation. Note: Records for SEQ ID No 2110 (AAK52581), 2111 (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the sequence listing were missing at the time of publication
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Human, cytokine, cell proliferation, cell differentiation, gene therapy, vaccine, peptide therapy, stem cell growth factor, haematopoiesis, tissue growth factor, immunomodulatory, cancer, leukaemia, nervous system disorder, arthritis, inflammation, ss.

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Human polynucleotide SEQ ID NO 2079

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(first entry)

06-NOV-2001

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This invention describes novel human ceramidase (I) containing a specific attructural motif which has antiproliferative, anticancer, anti-eczema, antipsoriasis and dermatological activity. (I) cleave ceramide, resulting in formation of sphingosine. (I), or the nucleic acid (II) encoding it, are used for diagnosis, prevention or treatment of diseases associated with ceramide defects, particularly altered cell proliferation (cancer) or altered ceramide layers on the skin (neurodermatitis, eczema, psoriasis), also for targeted modification of the permeability barrier by cubstances. Specifically they are used for diagnosis of ichthyosis, particularly lamellar ichthyosis ICR2. (I) can also be used in cosmetics. This sequence encodes human ceramidase XI
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                                                                                                                       specific structural motif, useful for treatment of ceramidase defects, e.g.
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Mismatches:
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59.38%
40.23%
36.34%
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diagnosis, prevention and
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                                                                   WPI; 2001-483256/52.
P-PSDB; AAB86363.
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US-10-017-410-2 (1-275) x ABL24043 (1-537)

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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16175-ABL30511), processed DNA ABB72072). The sequence data for this parent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                              208 ofyrieuHisCysValTrpHisIleLeuIleCysLeuAlaSerTyrLeuGlyCysValCy 228
                                                                                 228 sPheAlaTyrPheAspAlaAlaSerGluIleProGluGlnGlyProValIleArgPheTr 248
                                                                                                                                                      CATGGCCTTGGTGGATGCCAACTATGAGATGCCAGGTGAAACCCTCAAAGTCCGCTACTG 728
                 aLeuPheCysTrpIleSerAspGlnAlaPheCysGluLeuLeuSerSerPheHisPhePr 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell interactions.
                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila; developmental biology; cell signalling; insecticide; pharmaceutical; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                Drosophila melanogaster genomic polynucleotide SEQ ID NO 23602.
                                                                                                                                                                                                 pProSerGluLysTrpAlaPheIleGlyValProTyrValSerLeu 263
                                                                                                                                                                                                                    GCCTCGGGACAGTTGGCCC---GTGGGGCTGCCTACGTGGAAATC 771
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11-JUL-2000; 2000US-00614150
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Alignment Scores:

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228
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7 TrpAspHisLeuArgAlaGlySerSerGluValAspTrpCysGluAspAsnTyrThrlle
                      49 TGGGAGCACCTAAGACCCGGAAGCTCGCCGTCGACTGCTGCGAAGGCCAACTACTTGATT
                                          27 ValProAlaileAlaGluPheTyrAsnThrIleSerAsnValLeuPhePheIleLeuPro
                                                                                                                                           Drosophila; developmental biology; cell signalling; insecticide;
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23-MAR-2000; 2000US-0191637P.
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                                                                                           (PEKE ) PE CORP NY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Orosophila melanogaster genomic polynucleotide SEQ ID NO 42769
                                                                                                                                                      Sequence 4758 BP; 1304 A; 981 C; 980 G; 1493 T; 0 U; 0 Other;
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Claim 1; SEQ ID NO 23599; 21pp + Sequence Listing; English.
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Matches:
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Drosophila melanogaster.

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                                                                                                                                                                                                                                                                  The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and call-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL1676-ABL30511), expressed DNA sequences (ABL16176) and the encoded proteins (ABBS7737-ABR27072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pot_sequences
                                                             New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
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                                                                                                                                                                                                       Claim 1; SEQ ID NO 42769; 21pp + Sequence Listing; English.
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3355, Ap 5, Appli Appli , Appl

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APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: No. 6783969el Nucleic Acids and
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 803
CURRENT APPLICATION NUMBER: US/09/799,451
CURRENT FILING DATE: 2001-03-05
NUMBER OF SEQ ID NOS: 948
SOFTWARE: pt_FL_genes Version 2.0
SEQ ID NO 875
LENGTH: 1063
US-09-540-236-426
US-08-956-171R-63
US-08-91-986A-63
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Ma, Yunging
Yamazaki, Victoria
Chen, Rui-hong
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Zhou, Ping
Goodrich, Ryle
Asundi, Vinod
Ren, Feiyan
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Xue, Aidong J.
Zhao, Qing A.
Wang, Jian-Rui
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Yang, Yonghong
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Ghosh, Reena
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-MODEL=frame+ p2n.modlel -DEV=xlp
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                       GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-621-976-11241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       134 AlaileThrThrCysLeuAlaPheileLysProAlaileAsnAsnileSerLeuMetile 153
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218 GTAGGAATGGGATCCTGGTGCTTCCACATGACTCTGAAATATGAAATGCAGCTATTGGAT
                                                                                                                                                                                                                                                           34 TyrAsnThrIleSerAsnValLeuPhePheIleLeuProProIleCysMetCysLeuPhe
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RESULT 2 2.09-621-976-11241/c ; Sequence 11241, Application US/09621976 ; Patent No. 6639063

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APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: 107196.132
CURRENT APPLICATION NUMBER: US 60/074,725
PRIOR FILING DATE: 1998-02-13
PRIOR PLING DATE: 1998-02-13
PRIOR PLING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 1441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      145 TIGAATACTACCACTAACTCAGTATTTATTGCTTTGGCAAC-ATTTGGGATATATCATGC 203
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                                                                                                                                                                                                                                                                                                                                                                                                                        MetGlyAlaProHieTrpTrpAspHieLeuArgAlaGlySerSerGluValAspTrpCys
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APPLICANT: Jobert, S.
APPLICANT: Glochano, J.Y.
TITLE REFERENCE: GENSET. 054PR2
CURRENT APPLICATION NOMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 11241
LENGTH: 358
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Matches:
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Sequence 1441, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION;
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173.00
40.64%
27.09%
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204.00
97.30%
91.89%
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Best Local Similarity:
Query Match:
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Best Local Similarity:
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US-09-248-796A-1441
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ATTORNEY/AGENT INFORMATION: NAME: COllins, John M. REGISTRATION NUMBER: 25.04; REFERENCE/DOCKET NUMBER: 25.04; TELECOMMUNICATION INFORMATION: TELEPHONE: 816/474-9057 INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS: LENGTH: 6755 base pairs TYPE: nucleic acid STRANDEDNESS: double TOPOLOGY: unknown MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO ANTI-SENSE: NO ORAGINAL SOURCE: ORGANISM: Staphylococcus aurei JENGTH: SENSE: NO RIGINAL SOURCE: ORGANISM: Staphylococcus aurei STRANISM: UT0007	Alignment Scores: 0.00729 Pred. No.: 0.00729 Score: 118.50 Percent Similarity: 31.19% Best Local Similarity: 21.54% Query Match: 3	-10-017-410-2 (1-275) x 42 PhePheIleLe 3259 TTCTTTGTCGT	Oy 54 ArgdinTyrAlaThrCysbhaAsi Db 3199 TGGCTGTTGGCGTTTGTTTTC Oy 74 Val	75	Db 3088 CCCCCTTTGCTGCCCTGGGTTCC Qy 87 PheLeuGlyGlnMetLeuAspGln Db 3028 CTGCTTGTGCCCCTCTTTTCT Qy 107 MetTrpPheProArgArgTyrLee Db 2968 TCTTTTTCTCTCTCTCTGCTG Qy 126 Db 2911 TGTTCTTTTTGTTGCTGCTGCTG Qy 135 IleThrThrCGTTGCCGTCGCC Qy 135 IleThrThrCGTTGCCGTCGCCTGC Qy 135 IleThrThrCGTTGCTCTTCTTTTG Qy 144 ProAlalleAshAshIleSerLee Db 2791 CCCCTGTGTTTTTTTTTT Qy 164 AlaGluLeuLysArgCysAspAst Db 2731 TTT
Oy ::: Db :::	OY 144 OAJAIIEASAABANIESETLEUMETIIELEUGIYLEUPTOCYSTHRAIALEULEUVA 163	174 PheLysLeuGlyLeuPheSerGlyLeuTrpTrpThrLeuAlaLeuPheCysTrpIleSe 19 :	Db 630 TGACATTCATTTTGTGATTTTGCTGCTACCAGACGAGAATGGGGTATTCCATATGG 689 Qy 210LeuHisCysValTrpHisIleLeuIleCysLeuAlaSerTyrLeuGl 225 Db 690 GTTGTCTTGGAAGGACACGGATGGGTGGTGACATATTCACTGGGATTGGTGTCTACTATTC 749 Qy 225 yCysVal	750 TITGGIGIAIGAAGAGIAITIGGGCIGITIC 78	RESULT 4 US-08-931-99-4/C US-08-931-999-4/C Sequence 4, Application US/08931999 Fatent No. 643219 GENERAL INFORMATION: FAPLICANT: Tandolo, John J. APPLICANT: Crupper, Scott S. TITLE OF INVENTION: Broad Spectrum Chemotherapeutic Peptide NUMBER OF SEQUENCES: ADDRESSEE: Hovey, Williams, Timmons & Collins STREET: 2405 Grand Boulevard, Suite 400 CITY: Kansas City STATE: Missouri COUNTRY: U.S.A. ZIP: 64108 MISSOURI COMPUTER READABLE FORM: MISSOURI COMPUTER READABLE FORM: MISSOURI SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/931,999 FILING DATE: 19-SEP-1996 FILING DATE: 19-SEP-1996

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snSerGlylleTyrLeulleTrpThrLeuLeuValVal 73
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CG-----TTTCTTGTGTTCCCCCTTCTTTTCCTT 3149
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Matches:
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Mismatches:
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109 PhebroAlgArgTyTieu	1 (1-2859) TYRALATHE TRACGCGCC TRACGCGCCC TRACGCGCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC
2070 ———————————————————————————————————	0y 63 GlylleTyrLeuValVal 73 bb 602 TTCCTTCTCCTCTCGCTACGCAGCCACCTATGCTGGTACCACTCTGG 661 Cy 74 ValGlylleGlySerValTyrPheHisAlaThrLeuSerPheLeuGlyGlnMet 91 ::: ::: ::: ::: :::

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APPLICANT: PXE International, Inc.
APPLICANT: PXE International, Inc.
APPLICANT: PXE International, Inc.
APPLICANT: University of Hawaii
TITLE OF INVENTION: Mutations in a gene encoding an ABC transporter (MRP6) causing
TITLE OF INVENTION: Pseudoxanthoma Elasticum
FILE REFERENCE: PXE-001
CURRENT APPLICATION NUMBER: US/09/792,616
CURRENT FILING DATE: 2001-02-23
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PATENTIN Version 3.0
                                                                       1377 TTCCCGCGCCTCGACCGCTTCCTCCGCGGCCTGCTGCTGCGCGTGGTCGTCGTTGGCC 1318
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                                                     TyrieuIleTrpThrieuLeuValValValGlyIleGlySerValTyrPheHisAlaThr
                                                                                                                                                                                                                                                                     115 ---ProLysIlePheArgAsnAspArgGlyArgPheLysAlaValValCysValLeuSer
                                                                                                                           LeuSerPheLeu-----GlyGlnMetLeuAspGluLeuAlaIleLeuTrpValLeuMet
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        206 HisPheProTyrLeuHisCysValTrpHisIleLeuIleCysLeuAlaSerTyrLeuGly
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                    US-10-017-410-2 (1-275) x US-09-252-991A-1139 (1-1575)
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OTHER INFORMATION: "n" can be an A or a T
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38.91%
24.73%
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ORGANISM: Homo sapiens
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Best Local Similarity:
Query Match:
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LENGTH: 107820
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERBNCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR PILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
SEQ ID NO 1139
LENGTH: 1575
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               195 AspGlnAlaPheCysGluLeuLeuSerSerPheHisPheProTyrLeuHisCysValTrp 214
                                                                                        GlyArgPheLysAlaValValCysValLeuSerAlaIleThrThrCysLeuAlaPheIle 142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      215 HisIleLeuIleCysLeuAlaSerTyrLeuGlyCysValCysPheAlaTyrPheAspAla 234
                                                                                                                                        92 LeuAspGluLeuAlaIleLeuTrpValLeuMet------CysAlaLeuAlaMetTrp 108
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                               576 TICCICITCGICICGCTACGCGAGGCCACCTAIGCCIGGIACCIGCIGIACAACCICAGC 735
                                                              74 ValGlylleGlySerValTyrPheHisAlaThrLeuSerPheLeu-----GlyGlnMet 91
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; Sequence 1139, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
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                                                                                                                                                                                                            PheProArgArgTyrLeu----
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ORGANISM: Acinetobacter baumannii
                                                                                                                           Percent Similarity:
Best Local Similarity:
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                                  us-09-328-352-577
                                                                        Alignment Scores:
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TYPE: DNA
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Retent No. 6562958

GRNERAL INFORMATION:
GRNERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 577
LENGTH: 1794
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                                                                           38295 TTCTGTCCTTATAATGCTACTGTTATG-----TTGCTGGAATTTTGCCATCATGTTACT 38348
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                                                     19 TrpCysGluAspAsnTyrThrIleValProAlaIleAlaGluPheTyrAsnThrIleSer
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                                                                                                                           39 AsnValleuPhePheIleLeuProProIleCysMetCysLeuPheArgGlnTyrAlaThr
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                    US-10-017-410-2 (1-275) x US-09-792-616-1 (1-107820)
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                                                                                                                                                                                                                                                                                                                        91 MetLeuAspGluLeuAlaIleLeuTrpValLeuMetCysAlaLeuAlaMetTrpPhePro 110
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TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REPERENCE: PU3480US
CURRENT APPLICATION NUMBER: US/09/710,279
CURRENT FILING DATE: 2000-11-09
PRIOR APPLICATION NUMBER: 60/164,258
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                                                             Conservative:
Mismatches:
Indels:
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   Length:
Matches:
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; Sequence 4182, Application US/09710279
; Patent No. 6703492
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US-09-248-796A-2470
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GlyLeuPheSerGlyLeuTrpTrpThrLeuAlaLeuPheCysTrpIleSerAspGlnAla 197
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        221 aSerTyrLeu-GlyCysValCysPheAlaTyrPheAspAlaAlaSerGluIleProGluG 241
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                                                                                                                                                                                                                                                                                                                 ValProAlaileAlaGluPheTyrAsnThrileSerAsnVal---LeuPhePheileLeu 45 :::
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                                                                                                                                                                                                                                                                                                                                                                 ProProlleCysMetCysLeuPheArgGlnTyrAlaThrCysPheAsnSerGlyIleTyr 65
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                                                                                              OTHER INFORMATION: Description of Artificial Sequence: synthetic OTHER INFORMATION: nucleic acid sequence
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68
38
92
112
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Matches:
Conservative:
Mismatches:
Indels:
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                                                            TYPE: DNA ORGANISM: Artificial Sequence
PRIOR FILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 4182
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98.50
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Best Local Similarity:
Query Match:
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                                                                                                                      US-09-710-279-4182
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                                               LENGTH: 3304
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---SerG 251
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TrpCysGluAspAsnTyrThrIle-ValProAlaIleAlaGluPheTyrAsnThrIleSe 38
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              231 ATGTAAAGTGGAATGGGAGCATTTCCATAAGTTTTTTCAACAAAAGTACCTATCTCAGACC
                                                                                                                                                                                          251 luLysTrpAlaPheIleGlyValProTyrValSerLeuLeuCysAlaHisLysLysSer-
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Mismatches:
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241 lnGlyProValIleArgPheTrpPro-
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291 TATTTTGATTTCGCTTGTT
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ORGANISM: Candida albicans
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Best Local Similarity:
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Sequence 26, Application US/09540236

Patent No. 6673910

GENERAL INFORMATION:

APPLICANT: GATY L. Breton et al.

ITILE OF INVENTION: POR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: POR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: POR DIAGNOSTICS AND THERAPEUTICS

CURRENT APPLICATION NUMBER: US/09/540,236

CURRENT FILING DATE: 2000-04-04

NUMBER OF SEQ ID NOS: 3840
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89610 G----TTATGGCAAGCAGGATTTTGGTTG---TCATTTATTGCCGTGTTGTTATTGAT 89660
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                                                       132 uSerAlaIleThrThrCysLeu----AlaPheIleLysProAlaIleAsnAsnIleSe 150
                                                                                                                               150 rieuMetileLeuGlyLeuProCysThrAlaLeuLeuValAlaGluLeuLysArgCysAs 170
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                                                                                                                                                                                                                                                                                                                                                                                                                              ----SerGluIleProGluGlnGlyProVa 244
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                                                                               936 GTATCAATTGGCAGG---TATTTC-----GCATTTGCTTGCCATTTCAGGGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99661 GCATTATGAGTCACCCAAAATTGATATGATCAATGATACCAATCAAAATCAGGGGCAACT
                                                                                                                                                                                                                                                                             190 eCysTrplleSerAspGlnAlaPheCysGluLeuLeuSerSerPheHisPheProTyrLe
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                                                                                                                                                                   ----GCAGCTTGGCTGGTTCGCTACTTA
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Conservative:
Mismatches:
Indels:
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38.68%
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6.42%
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US-09-540-236-426
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Best Local Similarity:
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T.FNGTH: 2304
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Pred. No.:
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APPLICANT: Patterson, Chandra
APPLICANT: Patterson, Chandra
APPLICANT: Berg, Kim, L.
TITLE OF INVENTION: NUCLECTIDE SEQUENCES OF MORAXELLA CATARRHALIS GENOME
FILE REPERENCE: PM-0008-4 US
CURRENT APPLICATION NUMBER: US/09/596,002
CURRENT PILING DATE: 2000-06-16
PRIOR PILING DATE: 1999-06-18
NUMBER OF SEQ ID NOS:
SOFTWARE: PERL Program
SOFTWARE: PERL Program
SOFTWARE: PERL Program
SOFTWARE: PARO 336
TYPE: NUMBER: ON 336
TYPE: NUMBER: ON 336
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                                                                                                                                                he-SerGlyLeuTrpThrLeuAlaLeuPheCysTrpIleSerAspGlnAla---Phe 198
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 -LeuGlyLeuProCysThrA 160
                   ---TGTTTCATATTCGATAGTTGCAAAGAG
                                                                                                                                                                                                                                                                                             218 IleCysLeuAlaSerTyrLeuGlyCys---ValCys-PheAlaTyrPheAspAlaAlaSe
                                                                                                                                                                                                                                                                                                                                                                      236 rGluIleProGluGlnGlyProValIleArgPheTrpProSerGluLysTrpAlaPheIl
                                                                         160 laLeuLeuValAlaGluLeuLysArgCysAspAsnValArgValPheLysLeuGlyLeuP
                                                                                                                                                                                                                       CysGluLeuLeuSerSerPheHisPheProTyrLeuHisCys---ValTrpHislleLeu
                                                                                                                                                                                                                                                            -------rcrrggrgrgrgrrgrrgrrarragarrracan
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Matches:
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Mismatches:
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720 TGGATTGTTGTACTATTATTGTT 744
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S-09-596-002-36
Sequence 36, Application US/09596002
Patent No. 6632636
GENERAL INFORMATION:
APPLICANT: Lagace, Robert, E.
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97.50
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6.45%
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OTHER INFORMATION: Incyte
PUBLICATION INFORMATION:
                                                                                                                                                                             564 TCCAATIGACTCTGG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: M. catarrhalis
                                                                                                                                                                                                                                                                                                                                                                                                           684 TAAGTTG----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----ArgPheLysAlaValValCysValLeuSerAlaIleThrThrCysLeuAla 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            141 PhelleLysProAlalleAsnAsnIleSerLeuMetIleLeuGlyLeuProCysThrAla 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 SerGlyLeuTrpTrpThrLeuAlaLeuPheCysTrpIleSerAspGlnAlaPheCys--- 199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 SerAsnValLeuPhelleLeuProProlleCysMetCysLeuPheArg---GlnTyr 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  57 AlaThrCys-----PheAsnSerGlyIleTyrLeuIjeTrpThrLeuLeuValValVal
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                     63:
                                                                                                                                                   TOPOLOGY: linear SEQUENCE DESCRIPTION: SEQUENCE
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; Sequence 63, Application US/08781986A
; Patent No. 6737248
  (240) 314-1224
                      TELEFAX: (301) 309-8439 INFORMATION FOR SEQ ID NO: 63: SEQUENCE CHARACTERISTICS:
                                                                                   LENGTH: 8155 base pairs
                                                                                                         TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Charles Kunsch
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    TELEPHONE:
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APPLICANT: Charles
                                                                                                                                                                                                                                                                                                                      Similarity:
                                                                                                                                                                                                                                                                                                Percent Similarity:
                                                                                                                                                                                           US-08-956-171E-63
                                                                                                                                                                                                                                       Alignment Scores:
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Patrick S. Dillon
Craig A. Rosen
Steven C. Barash
Michael R. Fannon
TITLE OF INVENTION: Staphylococcus aureus Polymucleotides and Sequences
NUMBER OF SEQUENCES: 5256
                                                                                                                                                                                                                                                                                                                                                                                                                             1319
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.041 TGCACAACACATTTATGCACATTTGCCAAGATGGCAAATTCGTATGATGGTCATGGTGTT 1100
                                                                                 1101 GGCAAGTTTGGTTTATGCGTTGTTACAGGGTTTGATGTGCCTGCGGGGGGGAACTGTTTA 1160
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                                                                                                                                                                                                              pAsnValArgValPheLysLeuGlyLeuPheSerGlyLeuTrpTrpThrLeuAlaLeuPh 190
                                                                                                                                                                                                                                                                                                                                                                                 210 uHisCysValTrpHisIleLeuIleCysLeuAlaSerTyrLeuGlyCysValCysPheAl 230
                                            uSerAlalleThrThrCysLeu-----AlaPhelleLysProAlalleAsnAsnIleSe 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---TrpAlaPhelleGlyValPr 259
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                                                                                                                           rLeuMetIleLeuGlyLeuProCysThrAlaLeuLeuValAlaGluLeuLysArgCysAs
                                                                                                                                                 |||:::|||
|161 TITATTAATT------GCAGCTTGGCTGGTTCGCTA-------
                                                                                                                                                                                                                                                                                                190 eCysTrpIleSerAspGlnAlaPheCysGluLeuLeuSerSerPheHisPheProTyrLe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     230 aTyrPheAspAlaAlaSerGluIleProGlu------GlnGlyProVallleAr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33 OPERATING SYSTEM: MSDGS version 6.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1440 ACCTGTGTCTATCTTATTTGGCAAGGTATCA 1473
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STREET: 9410 Key West Avenue
CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/956,171E
FILING DATE: 20-OCE-1997
CLASSIFICATION: <Unknown>
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FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
FILING DATE: January 3, 1997
ATTORNEY/AGENT INFORMATION:
NAME: MARK J. Hyman
REGISTRATION NUMBER: 46,789
REFERENCE/DOCKET NUMBER: PB248P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          oTyrValSerLeuLeuCysAlaHisLysLysSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 63, Application US/08956171E Patent No. 6593114 GENERAL INFORMATION:
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5454 AGCAATIGCTICTITCGCATTAICTITAGTIGTIGCTGGCTGAAICGCTICAAITIT 5395
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               57 AlaThrCys-----PheAsnSerGlyIleTyrLeuIleTrpThrLeuLeuValValVal 74
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CORRESPONDENCE ADDRESS:
ADDRESSER: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
CITY: USA
CUTYRR: Naryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPREATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,986A
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                         FILING DATE:
CLASSIFICATION: 435
FRIOR APPLICATION: 435
FRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATORNEY/AGENT INFORMATION:
NAME: Benson, Bob
REGISTATION NUMBER: PB248PP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEPHONE: (301) 309-8512
INFORMATION FOR SEQ ID NO: 63:
ENGURATION FOR SEQ ID NO: 63:
TELEGITH: 8155 base pairs
TYPE: MUCLeic acid
STRANDENNESS: double
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ò	181	181 SerGlyLeuTrpThrLeuAlaLeuPheCysTrpIleSerAspGlnAlaPheCys 199	199
qq	5016	TGTTTAACGTTCACTTGTTTTTGAGCGATTTCCGCTTTTTGCACGATTTCCGCTTTTGCATC 4972	4972
δ	200	ysyy	212
QQ	4971	4971 CGATITICITAGITGIGGCAGCTIGAACTIGAITAAITGCAGCAAIACTAITGICITIAGC 4912	4912
ò	213	213 ValTrpHisIleLeuIleCysLeuAlaSerTyrLeuGlyCysValCysPheAlaTyrPhe 232	232
QQ	4911	4911 IGTIGITACAICACIGITIGIAITIGCAGCAICAAGAITIGITCITGCITCITGCITITT 4852	4852
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Title: Perfect score: Sequence:

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Scoring table:

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Sequence 30658, A
Sequence 30658, A
Sequence 17, Appl
Sequence 2014, Ap
Sequence 1743, Ap
Sequence 12701, A
Sequence 1369, Ap
Sequence 2099, Ap
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Sequence 151, App
Sequence 3, Appli
Sequence 6, Appli
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Publication No. US20020115094A1

GENERAL INFORMATION:

APPLICANT: Farnham, Peggy J

APPLICANT: Graveel, Carrie R

TITLE OF INVENTION: Polymouleotide Differentially Expressed in Liver Cancer;

FILE REFERENCE: 960296.97401

CURRENT APPLICATION NUMBER: US/10/017,410

CURRENT FILING DATE: 2001-12-14

NUMBER OF SEQ ID NOS: 4

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 1
                                                                                                                                      Sequence 4, Appli
Sequence 32295, A
Sequence 107231,
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; NAME/KEY: CDS
; LOCATION: (35)..(859)
US-10-017-410-1
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-MODEL=frame+ p2n.model -DEV=xlp
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-DB=Published Applications NA -OFMT=fastap -SUFFIX=rnpb -WINMATCH=0.1
-LOOPELS - LOOPEXT=0 -UNITS=bite -STRAT=1 -END=-1 -WATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pct -NORM=ext -HBAPSIZE=500 -MINLEN=0
-MAXIEN=200000000 -USRE=US10017410 @CGN 1 1.723 @runat 19112004 133621_19052
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-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DBLOP=6 -DBLEXT=7
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1512
1 MGAPHWWDHLRAGSSEVDWC.....IGVPYVSLLCAHKKSPVKIT
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              GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Xgapop 10.0, Xgapext
Ygapop 10.0, Ygapext
Fgapop 6.0, Fgapext
Delop 6.0, Delext
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Maximum DB seq length: 200000000
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Database

92688, A 3107, Ap

615, App 35305, A 77895, A 1999, Ap

34549, A 111725,

875, App 77897, A

5, Appli

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## APPLICANT: ALS., watcasus
### APPLICANT: Bos Biotechnology, Inc.
#### APPLICANT: Bos Biotechnology, Inc.
#### ITILE OF INVENTION: Methods of Diagnosis of Bladder Cancer, Compositions
### ITILE OF INVENTION: and Methods of Screening for Modulators of Bladder
### ITILE OF INVENTION: Cancer
### ITILE OF INVENTION: Cancer
### CURRENT APPLICATION WUMBER: US/10/188,832
### CURRENT FILING DATE: 2001-07-03
### PRIOR APPLICATION WUMBER: US 60/330,814
### PRIOR APPLICATION WUMBER: US 60/330,99
### PRIOR FILING DATE: 2001-08-03
### PRIOR FILING DATE: 2001-08-03
### PRIOR FILING DATE: 2001-11-08
### PRIOR FILING DATE: 2001-11-08
### PRIOR FILING DATE: 2001-11-13
### PRIOR FILING DATE: 2001-11-13
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Query Match:
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; ORGANISM: Homo
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Mismatches:
Indels:
Gaps:
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                              Length:
Matches:
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US-10-188-832-21
; Sequence 21, Application US/10188832
; Publication No. US2040076955A1
; GENERAL INFORMATION:
; APPLICANT: Mack, David H.
                            4.29e-157
1512.00
100.00%
100.00%
                                                              Percent Similarity:
Best Local Similarity:
Query Match:
           Alignment Scores:
Pred. No.:
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256
14
5
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                   Matches:
Conservative:
Mismatches:
Indels:
                                                                           US-10-017-410-2 (1-275) x US-10-188-832-21 (1-4202)
                                                          Gaps:
2.63e-148
1433.00
98.18*
93.09*
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Query Match: 94.78* Indels: 0 DB: 15 Gaps: 0	US-10-017-410-2 (1-275) x US-10-295-027-151 (1-4212) Oy 1 MetGlyAlaProHisTrpTrpAspHisLeuArgAlaGlySerSerGluValAspTrpCys 20	Db ATGGGCCCCCGCACTGGTGGGACCAGCTGCAGGTCGGAGGTGGACTGGTGCTGGTGC 146 Qy 21 GluAspAenTyrThrIleValProAla1leAlaGluPheTyrAsnThrIleSerAsnVal 40	147 GAGGACAACTACACCATCGTGCCTGCTATCGCCGAGTTCTACAACACGGATCAGCAATGTC	Oy 41 LeuPhePheIleLeuProProIleCysMetCysLeuPheArgGlnTyrAlaThrCysPhe 60	AshSerGly11eTyrLeu11eTrpThrLeuLeuValValValGly11eGlySerValTyr	81	101 LeuwetCysAlaLeuAlawetTrpPheProArgArgTyrLeuProLysIlePheArgAsn 1	Oy 121 AspargGlyArgPheLysalavalValCysValLeuSerAlarleThrThrCysLeuAla 140	Oy 141 PhelleLysProAlaileAsnAsnIleSerLeuMetileLeuGlyLeuProCysThrAla 160	Oy 161 LeuLeuValalaGluLeuLysArgCysAspAsnValArgValPheLysLeuGlyLeuPhe 180	Oy 181 SerGlyLeuTrpTrpThrLeuAlaLeuPheCysTrpIleSerAspGlnAlaPheCysGlu 200	Qy 201 LeuleuSerSerPheHisPheProTyrLeuHisCysValTrpHisIleLeuIleCysLeu 220	Oy 221 AlaSerTyrLeuGlyCysValCysPheAlaTyrPheAspAlaAlaSerGluIleProGlu 240	Qy 241 GlnGlyProValIleArgPheTrpProSerGluLysTrpAlaPheIleGlyValProTyr 260	Qy 261 ValSerLeuLeuCysAlaHistysErProValLysIleThr 275	8	; APPLICANT: Graveel, Carrie R ; TITLE OF INVENTION: POLYMUCIECTION DIfferentially Expressed in Liver Cancer ; FILE REFERENCE: 960296,97401 ; CURRENT APPLICATION NUMBER: US/10/017,410 ; CURRENT FILING DATE: 2001-12-14 ; NUMBER OF SEQ ID NOS: 4
	Oy 201 LeuLeuSerSerbheHisPheProTyrLeuHisGysValTrpHisIleLeuIleGysLeu 220	Qy 221 AlaSerTyrLeuGlyCysValCysPheAlaTyrPheAspAlaAlaSerGluIleFroGlu 240	241 GlnGlyProvalIleArgPheTrpProSerGluLysTrpAlaPheIleGlyValProTyr	Db 797 CAAGGCCCTGTCATCAAGTTCTGGCCCAATGAGAAATGGGCCTTCATTGGTGTCCCTAT 856 Qy 261 ValSerLeuLeuCysAlaHisLysLysSerProValLysIleThr 275	Db 857 GTGTCCTCTGTGTGTGCCAACAAGAATCATCAGTCAAGATCACG 901	US-10-295-027-151 ; Sequence 151, Application US/10295027 ; Publication No. US20030232350A1 ; GENERAL INFORMATION:	APPLICANT: Afar, Daniel ; APPLICANT: Aziz, Natasha ; APPLICANT: Ginsberg, Wendy M. ; APPLICANT: Gish, Kurt C	; APPLICANT: Glynne, kichard ; APPLICANT: Mack, David H. ; APPLICANT: Mack, David H.	; APPLICANT: Watson, Susan K. ; APPLICANT: Bos Biotechnology, Inc. ; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and ; TITLE OF INVENTION: Methods of Screening for Modulators of Cancer			PRIOR PRIOR PRIOR	PRIOR PRIOR PRIOR	FRICK APPLICATION NUMBER: US 60/347,349 ; PRICK PILING DATE: 2002-01-10 ; PRICK PELICATION NUMBER: US 60/355,250 ; DRICK TILING DATE: 000.000000000000000000000000000000000	PRIOR PRIOR Remain		Alignment Scores: 2.64e-148 Length: 4212 Pred. No.: 2.64e-148 Length: 4212 Score: 1433.00 Matches: 256 Percent Similarity: 98.18\$ Conservative: 14 Best Local Similarity: 93.09\$ Mismatches: 5

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PhelleLysProAlalleAsnAsnIleSerLeuMetIleLeuGlyLeuProCysThrAla 160
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           825
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Matches:
Conservative:
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Indels:
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                                                 1.01e-142
1373.50
94.91%
89.45%
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US-10-182-447-6
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Best Local Similarity:
Query Match:
DB:
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15
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                                                                                                                    Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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                                                                                                                    4.15e-146
1404.00
96.73*
91.27*
92.86*
                             ; TYPE: DNA
; ORGANISM: Homo Bapiens
; FRATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(825)
US-10-017-410-3
                                                                                                                                        Percent Similarity:
Best Local Similarity:
SOFTWARE: Patentin
SEQ ID NO 3
LENGTH: 828
                                                                                                          Alignment Scores
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US-10-182-447-4
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Best Local Similarity:
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US-09-945-527-48

Sequence 48, Application US/09945527

Publication No. US20030055588A1

GENERAL INFORMATION:

APPLICANT: RObison, Keith E.

TITLE OF INVENTION: Nucleic Acid and Protein Homologs

TITLE OF INVENTION: Nucleic Acid and Protein Homologs

TITLE OF INVENTION: Nucleic Acid and Protein Homologs

CURRENT FILING DATE: 2001/237985

CURRENT FILING DATE: 2001-08-29

NUMBER OF SEQ ID NOS: 65

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 48
                                                                                     240
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                                        AlaSerTyrLeuGlyCysValCysPheAlaTyrPheAspAlaAlaSerGluIleProGlu
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                                                                                                        658 GCTGCCTACCTGGGTGTATGCTTTGCCTACTTTGATGCTGCCTCAGAGATTCCTGAG
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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91.73%
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US-09-945-527-48
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Best Local Similarity:
Query Match:
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Pred. No.:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           148 nIleSerLeuMetIleLeuGlyLeuProCysThrAlaLeuLeuValAlaGluLeuLysAr 168
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                         637 GAC------CGATACCCACCACCATGATGCTTTCT
121 AspArgGlyArgPheLysAlaValValCysValLeuSer
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Mismatches:
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Matches:
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Publication No. US20030185814A1

GENERAL INPORMATION:

APPLICANT: HOFMANN, KAY

TITLE OF INVENTION: CERAMIDASE

FILE REFERENCE: P68055USO

CURRENT APPLICATION NUMBER: US/10/182,447

CURRENT FILING DATE: 2002-07-29

PRIOR APPLICATION NUMBER: DE 10003293.1

PRIOR FILING DATE: 2000-01-27

PRIOR FILING DATE: 2000-01-27

PRIOR FILING DATE: 2000-01-27

PRIOR FILING DATE: 2000-01-27

PRIOR FILING DATE: 2000-03-09

NUMBER OF SEQ ID NOS: 14

SOFTWARE: PALENTIN VET: 2.1

LENGTH: 792
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Sequence 107231, Application US/10425115
PUBLICANT: US20040214272A1
GENERAL INFORMATION: Thomas J.
APPLICANT: APPLICANT: A Rosa, Thomas J.
APPLICANT: APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Plants
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(5322)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT PILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 107231
                                        684 CCGCAGGGGCACGCGTGGTGGCACGTGCTTATGGGCCTCCAACTCGTACTACTACAACACG 743
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                                                                                                                     468 GTACATTTCTTTGCCCGGTTCCAAGTCGTATTC-------AAGCTGCATTAC 512
                                                                                                                                                     149 IleSerLeuMetIleLeuGlyLeuProCysThrAlaLeuLeuValAlaGluLeuLysArg 168
                                                                                                                                                                          169 CyaAspAsnValArgValPheLysLeuGlyLeuPheSerGlyLeuTrpThrLeuAla 188
                                                                                                                                                                                                                                            573 GTGGGTGCGAAGCGGCTCGCAAACTGTGGGTC-----CTTACACTGACCCTTGG 623
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Matches:
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Mismatches:
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Best Local Similarity:
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ORGANISM: Zea mays
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APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Number: US/10/425,114
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
                                                aleuPheCysTrpIleSerAspGlnAlaPheCysGluLeuLeuSerSerPheHisPhePr 208
                                                                                                                   oTyrieuHisCysValTrpHisIleLeuIleCysLeuAlaSerTyrLeuGlyCysValCy 228
                                                                                                                                       609 CTATCTGCACAGCATCTGGCATGTGCTCATCACCTTCCCTTATGGCATGGTCAC 668
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GACCAGCAATAAGGAGCTTCGGCACCTGATTGAGGTCTCCGTGGTTTTATGGGGCTGTTGC
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TCTGACCAGCTGGATCAGTGTGACCGTCTGCAGCTTCTGGCAGGATTCATTTCTT
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Mismatches:
Indels:
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US-10-425-114-32295
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Matches:
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Sequence 32295, Application US/10425114

Publication No. US20040034888A1

GRNERAL INFORMATION:

APPLICANT: Liu, Jingdong
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43.73%
28.90%
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ORGANISM: Zea mays
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TTCCGCCAA------GGTTTTGAGAAACGGTTCAGTGTCTCACGTATCAGTATCCAATATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  208 ---ProTyrLeuHisCysValTrpHisIleLeuIleCysLeuAlaSerTyrLeuGlyCys
                                                                                                                                                                                                                                                                                                     SerSerGluValAspTrpCysGluAspAsnTyrThrIleValProAlaIleAlaGluPhe
                                                                                                                                                                                                                                                                                                                                                    513 ACGTCAACGACTGAGTTGTGCGAGGAGAATTATGCACACTCATCATATATCGCAGAATTC
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961 GTAGTICATITCTTTGCCCGGTTCCAAGTTGTATTC-----
                                                                                                Matches:
Conservative:
Mismatches:
Indels:
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US-10-437-963-42300
Sequence 42300, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
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                                                                                             213.50
43.56%
29.92%
14.12%
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Best Local Similarity:
JS-10-767-701-12261
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Fublication No. US20040172684A1

GENERAL INFORMATION:

SAPLICANT: Kovalic, David K.

APPLICANT: Zhou, Yihua

APPLICANT: Zhou, Yihua

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Plante and Uses Thereof For Plant Improvement

FILE REFERENCE: 38-21 (53535)

CURRENT APPLICATION NUMBER: US/10/767,701

KUMBER OF SEQ ID NOS: 63128

SEQ ID NO 12261

LENGTH: 1547
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                       TyrAsnThrIleSerAsnValLeuPhePheIleLeuProProIleCysMetCysLeuPhe
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 ::::: TGGTACGTCAACCCACAAGGGCATGGTGGCATATTCTCATGGGATTTAACTCATAC
                                                     224 LeuGlyCysValCysPheAlaTyrPheAspAlaAlaSerGluIleProGluGlnGlyPro
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Mismatches:
Indels:
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Matches:
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Publication No. US20030185814A1

GENERAL INFORMATION:

APPLICANT: HOFMANIN, KAY

APPLICANT: RADT, Marcus

TITLE OF INVENTION: CERAMIDASE

FILE REFERENCE: P68055USO

CURRENT APPLICATION NUMBER: US/10/182,447

CURRENT FILING DATE: 2002-07-29

PRIOR FILING DATE: 2000-01-27

PRIOR APPLICATION NUMBER: DE 10003293.1

PRIOR FILING DATE: 2000-01-27

PRIOR APPLICATION NUMBER: DE 1001392.3

PRIOR FILING DATE: 2000-03-09

NUMBER OF SEQ ID NOS: 14

SOFTWARE: PATENTIN VENTION NUMBER: DE 10011392.3

LENGTH: 801
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40.89%
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ORGANISM: Homo sapiens
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Best Local Similarity:
Query Match:
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                                                   APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Wu, Wei
APPLICANT: Buckharv, Andrey A.
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
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590 TACGGIGCTGTTTTGCAGTAGTCCATTTCCTGGTGCGATTCCAAGTGGTATTCAAG--- 646
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: Clone ID: PAT_MRT4530_45566C.1
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212.50
42.70%
27.34%
14.05%
La Rosa, Thomas J
Kovalic, David K
Zhou, Yihua
Cao, Yongwei
                                                                                                                                                                                                                                                                                 TYPE: DNA ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent Similarity:
Best Local Similarity:
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LENGTH: 1436
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APPLICANT: La Rosa, Thomas J.
APPLICANT: La Rosa, Thomas J.
APPLICANT: Availe, David K.
APPLICANT: Applicant Sou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Plants
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21 (53222) B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 77897
LENGTH: 1429
                  44 ACCTCCACGCTGGACTGCTGCGAGAGAACTACTCCGTGACCTGGTACATCGCCGAGTTC 103
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278 GAACTCCCAATGATATAC---AGCTGTTGCATATTTGTGTACTGCATGTTTGAATGTTTC 334
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SerSerGluValAspTrpCysGluAspAsnTyrThr11eValProAla1leAlaGluPhe :::||| :::|||||||||||||
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518 GGACTGGGTTATACATCATTGGGTATATTTTATTGGGATTTTTATTTTGGATATATAGAT
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334 TATAGGCCAAAAGTGAAGTTTCTCTTT 760
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698 CTTTTCAGTTTGTAT------
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US-10-302-172-875

Sequence 875, Application US/10302172

Publication No. US20040053250A1

GENERAL INFORMATION:

APPLICANT: Tang, Y. Tom

APPLICANT: A.W., Aldong J.

TITLE OF INVENTION: Polypeptides

TITLE OF INVENTION: Polypeptides

TITLE OF INVENTION: NUMBER: US/10/302,172

CURRENT APPLICATION NUMBER: US/10/302,172

CURRENT APPLICATION NUMBER: US/10/302,172

CURRENT APPLICATION NUMBER: PCT US/25,251

PRIOR PILING DATE: 2002-11-21

PRIOR PILING DATE: 2002-03-05

PRIOR PILING DATE: 2002-03-05

PRIOR PILING DATE: 2001-03-05

NUMBER: OF SEQ ID NOS: 950

SEQ ID NO 875

LENGTH: 1063

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         134 AlalleThrThrCysLeuAlaPhelleLysProAlalleAsnAsnIleSerLeuMetIle 153
                                                  394 GTAACCACAGTTTACCTTAAGGTAAAAGAGCCAATATTCCATCAGGTCATGTATGGAATG 453
                                                                                              LeuGlyLeuProCysThrAlaLeuLeuValAlaGluLeuLysArgCysAspAsnValArg 173
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CTTTTCAGTTTGTAT------
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ORGANISM: Homo sapiens
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Best Local Similarity:
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; LOCATION: (2)
US-10-302-172-875
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50 MetCysLeuPheArgGlnTyrAlaThrCysPheAsnSerGlyIleTyrLeuIleTrpThr 69
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      Sequence 2429, Application US/10017161
PUBLICATION NO. US20030143668A1
FUBLICANT: SURVA, MAKIKO
APPLICANT: AKATION,
APPLICANT: AKIYAMA, YUTSHI
TILLE OF INVENTION NOVEL G PROTEIN-COUPLED RECEPTORS
TILLE OF INVENTION NOWEL G PROTEIN-COUPLED RECEPTORS
CURRENT APPLICATION NUMBER: US/10/017,161
CURRENT FILING DATE: 2002-12-18
FRIOR PEPLICATION NUMBER: JP 2001/246789
FRIOR PEPLICATION NUMBER: JP 2001/246789
FRIOR PEPLICATION NUMBER: JP 2001/246789
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FRIOR PEPLICATION NUMBER: JP 2001/246789
FRIOR PEPLICATION NUMBER: JP 2001/246789
FRIOR PERIOR FILING DATE: 2001-06-18
NUMBER OF SEQ ID NOS: 2430
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 2428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-017-410-2 (1-275) x US-10-017-161-2429 (1-35425)
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Matches:
Conservative:
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LOCATION: (35270)..(35425)

OTHER INFORMATION: a, t, c, g, unknown or other
US-10-017-161-2429
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LOCATION: (35125)..(35225)
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LOCATION: (21462)..(21603)
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LOCATION: (23918)..(24055)
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                                                                                                                                                                                                                                                                                                          ORGANISM: Homo sapiens
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NAME/KEY: CDS
LOCATION: (201)..(293)
FEATURE:
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LOCATION: (1)..(35425)
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Best Local Similarity:
US-10-017-161-2429
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                204 SerPheHisPheProTyrLeuHisCysValTrpHisIleLeuIleCysLeuAlaSerTyr 223
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   90 GlnMetLeuAspGluLeuAlaIleLeuTrpValLeuMetCysAlaLeuAlaMet----- 107
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                                                                                                                                                                                                                                                                                     14 SerSerGluValAspTrpCysGluAspAsnTyrThrIleValProAlaileAlaGluPhe 33
                                                                                                                                                                                                                                                                                                                                                                                              71
                                                                                                                                                                                                                                                                                                                             34 TyrAsnThrileSerAsnValLeuPhePheIleLeuProProIleCysMetCysLeuPhe 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  54 ArgGlnTyrAlaThrCysPheAsnSerGlylleTyrLeuIleTrpThrLeuLeu-----
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Matches:
Conservative:
Mismatches:
Indels:
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                             ; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_171065C.1
US-10-425-115-77897
                                                                                                          1.23e-12
206.50
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1150 GTC 1152
 TYPE: DNA
ORGANISM: Zea mays
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                                                                                                  Alignment Scores:
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. E. I. (bases 1 to 1022).

E. I. (bases 1 to 1022).

National Institutes of Health, Mammalian Gene Collection (MGC).

L. Unpublished (1999).

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov.

Tissue Procurement: Dr. David Rowe cDNA Library Preparation: Invitrogen Corp.

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAMI467 row: j column: 05

High quality sequence stop: 681.
                                                                                                                                                       BU220481
BU203269
BI848265
CF169808
BX646596
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BF554219
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CB728612
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BU511164.1 GI:22817397
ENT.
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/clone="IMAGE:6505924"
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3355.970 Million cell updates/sec
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                                                                                                                                                                                                                                               US-10-017-410-2
1512
1 MGAPHWWDHIRAGSSEVDWC.....IGVPYVSLLCAHKKSPVKIT 275
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CA976684 A
AK085306 N
AY401890 I
CA463294 A
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AF370405 I
BUZ34223 6
                     GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                           using frame_plus_p2n model
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Maximum Match 100%
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AY401889
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BU234223
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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Match Length DB
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gb_htc...
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gb_gs811...
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Database :

1392 1230 1176 1176. 1163 1158.5 1110.5

Score

Result No.

EST 12-SEP-2002

BW216493 AMGNNUC:M BW351328

UI-R-A0-a CcLX06a22

AGENCOURT UI-R-E0-C

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681 bp DNA linear GSS 12-DEC-2003
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Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Rerriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, White, T.J., Sninsky, J.J., Inferring nonneutral evolution from human-chimp-mouse orthologous
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Direct Submission

Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering them based on alignment.

Location/Qualifiers
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Matches:
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Science 302 (5652), 1960-1963 (2003)
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/mol_type="genomic DNA"
/db_xref="taxon:10090"
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/locus_tag="HCM1041"
                                                                                                                                                                                Mus musculus (house mouse)
Mus musculus
                                                                          AY401891
Mus musculus HCM1041 ger
genomic survey sequence.
AY401891
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/tissue type="undifferentiated limb"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NHH MGC 114"
/note="Westor: PGWV-SPORT6.1; Site 1: EcoRV; Site_2: NotI;
/lone unidirectionally. Primer: Oligo dT. Average insert size 1.7 kb. Constructed by ResGen, Invitrogen Corp. Note: this is a NIH_MGC Library."
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Matches:
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Matches:

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AK085306
Mus musculus 0 day neonate Kidney DNA, RIKEN full-length enriched library, clone:D630008P07 product:similar to CANCER RELATED GENE-LIVER 1 [Mus musculus], full insert sequence.
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                               MetGlyAlaProHigTrpAspHigLeuArgAlaGlySerSerGluValAspTrpCys
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High-efficiency full-length cDNA
Meth. Enzymol. 303, 19-44 (1999)
9927923
                                                                                                 (1-868)
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AK085306.1 GI:26351558
HTC; CAP trapper.
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               Percent Similarity:
Best Local Similarity:
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Bukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Musna.
E 1 (bases 1 to 868)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
L Onpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Consortium (LINL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM1355 row: g column: 14
High quality sequence stop: 679.
                                                                                                                                                                                                                                                                                                                                                                                                                                             AGENCOURT 8877974 NCI CGAP Mam2 Mus musculus cDNA clone IMAGE:6437893 5', mRNA sequence.
CA976684.1 GI:27509338
EST.
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/note="Organ: mammary; Vector: pCWV-SPORT6; Site 1: Sall;
/note="Organ: mammary; Vector: pCWV-SPORT6; Site 1: Sall;
site 2: Not; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"
GACAATGTGCGTGTTTTAAGCTGGGCCTCTTCTCTGGCCTCTGGTGGACTCTGGCTCTC
                                                                                                             PheCysTrp1leSerAspGlnAlaPheCysGluLeuLeuSerSerPheHisPheProTyr
                                                                                                                                                                           LeuHisCysValTrpHisIleLeuIleCysLeuAlaSerTyrLeuGlyCysValCysPhe
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'dev_stage="5 months"
'lab_host="DH10B"
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clone="IMAGE:6437893"
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/strain="FVB/N-3"
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Mus musculus
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Pred. No.:
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CA976684
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Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,

868

cloning

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/codon_start=1
/protein_id="BA039416.1"
/brotein_id="BA039416.1"
/db_xref="G1:06351559"
/translation="MAAPHWWPHLRAGSSEVDWCEDNYTIVPAIAEFYNTISNVLFFI
LPPICMCLFRQYATCFNSGIYLIWTLLVVVGIGSYYFHATLSFLGQMLDELAILWVLM
CALAWWFPRRYLPKTFRNDRGRFKAVVCVLSAITTCLAFIKPAINNISLMILGLPCTA
LLVAELKRCDNVRVFKLGLFSGLWWTLALFCWISDQAFCELLSSFHFPYLHCVWSADR
G"
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Pan troglodytes HCM1041 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.
AY401890.1 GI:39757876
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(SPTR|AAL40408, evidence: FASTY, 100%ID, 77.8%length,
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Radachi, J., Alzawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayafak, M., Hizandar, T., Hiraoka, T., Hayafak, M., Hizandar, T., Hiraoka, T., Hayafak, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Kaya, S., Kunhara, C., Matsuyama, T., Miyazaki, M., Muza, M., Nowa, X., Kunhara, C., Matsuyama, T., Miyazaki, M., Muza, M., Nakamura, M., Nohi, K., Nowura, K., Ohno, M., Ohato, N., Sano, H., Saaki, D., Shibata, K., Shinagawa, A., Sakai, K., Sakarume, N., Sogabe, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, T., Takau, A., Tayawa, A., Takahashi, F., Takau-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Direct Submission and Hayashizaki, Y.

Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Submission and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomes Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gec.riken.jp, WEL: BL+45-503-9216)
  Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)
10499374
                                                                                                                                                          Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kahiwai, K., Pujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 1173)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The RIKEN Genome Exploration Research Group Phase II Team and
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Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)
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/clone_lib="gikEN full.length enriched mouse
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Please visit our web site for further details.
URL:http://genome.gsc.riken.jp/.
URL:http://fantom.gsc.riken.jp/.
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strain="CS7BL/6J"
/db_xref="FANTOM DB:D630008P07"
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TICTGCTGGATCAGTGACCGAGCTTTCTGCGAGCTGCTGTCATCCTTCAACTTCCCCTAC 480
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Jonathan Kuo, NIMH
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                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mamalia; Eutheria, Primates, Catarrhini, Hominidae, Pan. 1 (bases 1 to 681)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Perriera, S., Wang, G., Zheng, K.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
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This sequence was made by sequencing genomic exons and ordering them based on alignment.

Location/Qualifiers
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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/clone=lmAcms.cf710649.
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by oligo-dT priming and directionally cloned. 5' and 3'
adaptors were used in cloning as follows:
5'-AAGCAGTGGTATCAACGCGAGGGC3, and
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LeuHisCysValTrpHisIleLeuIleCysLeuAlaSerTyrLeuGlyCysValCysPhe
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Clark.A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Clark.A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wardy,G., Zheng,X.H., White,T.J., Shinsky,J.J., Adams,M.D. and Cargill,M. Direct Submission

Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering them based on alignment.

Location/Qualifiers
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                                                  ATGGGCCCCCCCCACTGGTGGGACCACCTGCGGCTGGCATTGGTGCATTGGTGC
                                                                                            GluAspAsnTyrThrIleValProAlaIleAlaGluPheTyrAsnThrIleSerAsnVal
                                                                                                               GAGGACAACTACACTATCGTGCCTGCCATTGCCGAGTTCTACAACACGATCAGCAACGTC
                                                                                                                                                          LeuPhePhelleLeuProProlleCysMetCysLeuPheArgGlnTyrAlaThrCysPhe
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Db 601 AATGAGAAATGGGCCTTCATTGGTGTCCCCTATGTGTCCCTGTGTGCCAACAAGAAA 660	Qy 270 SerProValLysileThr 275 	RESULT 8 AP370405 LOCUS DEFINITION Homo sapiens PP11646 mRNA, complete cds. ACCESSION AP370405 VERSION AP370405.1 GI:33341739	HTC HOM HOM Euk	ses 1 to 1527) Y., Zhou,X.M., Zhang,P.F F. and Gu,J.R. human cDNA clones with f	Growth JOURNAL Unpublished REFERENCE 2 (bases 1 to 1527) AUTHORS Zhang, P.P., Zhou, X.M., Jiang, H.Q., Huang, Y., Qin, W.X., Zhao, X.T.,	Wan, D.F. and G.V. K. TITLE Direct Submission JOURNAL Submitted (16-APR-2001) National Laboratory For Oncogenes & Related Genes, Shanghai Cancer Institute, 25/Ln 2200 Xie-Tu Road, Shanghai	• ' '	/molltype="mRNA" /db_xref="taxon:9606" CDS 218 .640 ctart=1	/product="PP11646" /protein_id="AAQ15241.1" /db_xref="G1:33341740" /db_xref="G1:33341740" /translation="MCLFRQYATCRNGIYLIWTLLVVVGIGSVYFHATLSFLGQMLD ELAVLWVLMCALAWMPPRRYLPKIFRNDRGRFKVVVSVLSAVTTCLAFVKPAINNISL MTLGVPCTPALLIABLKRHERNQRRHFRGGQQGGGRX"	ORIGIN	8.7e-104 1110.50 1110.50 66.20% 1 Similarity: 62.54% 5h: 3	4-6	57 AlaThrCysPheAsnSerGlyIleTyrLeulleTrpThrLeuLeuValValGlyIle	UY // GIYSETVALIYYFNEH18ALATNKLEUSEFPRELEUGLYGINMEKLEUASPGIULEUALA 96 	Qy 97 IleLeuTrpValLeuMetCysAlaLeuAlaMetTrpPheProArgArgTyrLeuProLys 116 :::	Qy 117 IlePheArgAsnAspArgGlyArgPheLysAlavalValValVsyValLeuSerAla1leThr 136

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Shultz,M.A., Zhang,L., Gu,Y.-Z., Baker,G.L., Fannuchi,M.V., Padua,A.M., Gurske,W.A., Morin,D., Penn,S.G., Jovanovich,S.B., Plopper,C.G. and Buckpitt,A.M. response to lung toxicants: I. Squencing and microarray development.

Squencing and microarray development.

Am. J. Respir. Cell Mol. Biol. 30 (3), 296-310 (2004)
Contact: Shultz MA.

Dept. of Molecular Biosciences, School of Veterinary Medicine University of California, Davis
1311 Haring Hall, One Shields Avenue, Davis, CA 95616, USA 752 0793
Fax: 530 752 0793
Fax: 530 752 4698
Rmail: mashultz@ucdavis.edu
Average Phred score is 20 or better. All poor quality data (Phred < 20) and vector/linker sequence has been removed.
High quality sequence stop: 565.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CF115220 555 bp mRNA linear EST 23-JUL-2003
Shultzomica08471 Rat lung airway and parenchyma cDNA libraries
Rattus norvegicus cDNA clone NP6159 5', mRNA sequence.
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Site_2: Not I; mRNA was isolated from microdissected rat
lung airways and parenchyma tissues."
                                                              480
                                                                                                                                    255
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              93
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                                                                                                                                 SerGluIleProGluGlnGlyProValIleArgPheTrpProSerGluLysTrpAlaPhe
                                                                                                                                                                       256 IleGlyValProTyrValSerLeuLeuCysAlaHisLysSerProValLysIleThr
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Matches:
Conservative:
Mismatches:

    .565
    /organism="Rattus norvegicus"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rattus norvegicus (Norway rat)
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CF115220.1 GI:33175919
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996.00
99.47%
96.28%
65.87%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rattus norvegicus
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Best Local Similarity:
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   216
                                                                  421
                                                                                                                                    236
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KEYWORDS
SOURCE
ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /dev stage="12"
/lab_host="blub."CSEQCHN5."
/lab_host="blub."CSEQCHN5."
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/note="Organ: heads, Vector: pBluescript II KS(+); Site_1:
/note="Organ: heads, Vector: pBluescript was
constructed from 1 million independent clones. CDNA
synthesis was initiated using an oligo(dT) primer, using
methylated C in the first strand synthesis reaction.
Following this first strand reaction, double-stranded cDNA
was blunted, ligated to NotI adapters, digested with
ECORI, size-selected, and cloned into the NotI and ECORI
compatible sites of a custom modified MCS of the
pBluescript (KS+) vector. The library was normalized in 2
rounds using conditions adapted from Soares et al., PNAS
(1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6
(1995): 791, except that a significantly longer
reannealing hybridization was used."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          155
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LysilePheArgAsnAspArgGlyArgPheLysAlaValValCysValLeuSerAlaile 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 ACTACCTGCCTTGCCTTCATTAAACCTGCCATCAACAACATCTCACTAA1GACTCTGGGGT 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GTTCCTTGCACAGCTTTACTCATTGCTGAGAGTGTGAGAGTGTGAAAAACCTGCGTGTGTAC 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LysLeuGlyLeuPheSerGlyLeuTrpTrpThrLeuAlaLeuPheCysTrp11eSerAsp 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GlnAlaPheCysGluLeuLeuSerSerPheHisPheProTyrLeuHisCysValTrpHis 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 GCTATICICIGGGICCTTATGTGTGCTTGCCATGTGGTTCCCTAGGAGATATCTACCA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 AGAGTTTTTCGAAATGACAGGAGCCGGTTTAAAGCTGCTGTTGGTGTCCTGTCTGGAGTT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LeuProCysThrAlaLeuLeuValAlaGluLeuLysArgCysAspAsnValArgValPhe 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAGCTTGGTCTGTTTCAGGTCTTTGGTGGATGCTAGCACTTTTCTGCTGGATCAGTGAC 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
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                                                                                                     of Science and Technology
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                             1. .698
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/db_xref="taxon:9031"
/clone="ChEST757k21"
                        Contact: Simon Hubbard
Department of Biomolecular Sciences
University of Manchester Institute of
(UMIST)
PO Box 89, Manchester, M60 1QD, UK
Tel: 0161208930
Fax: 01612360409
Email: Simon.Hubbard@umist.ac.uk.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (1-698)
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89.00%
66.20%
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Best Local Similarity:
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Pred. No.:
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PUBMED
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                               COMMENT
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Diete-"Site 1: Sal1; Site 2: BamH1; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)

(11), Pr-1771 (2000)

(11), Pr-1771 (2000)

Sugahara,Y. and Hayashizaki,Y. Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)

Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamanaka,I., Alzawa,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and
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                                                                                                                                                                                                                Hayashizaki,Y.
Computational Analysis of Full-Length Mouse cDNAs Compared with
Computational Sequences. Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp) for
further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue_type="kidney"
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/lab_host="DH10B"
/clone_lib="RIKEN full-length enriched, 0 day neonate
kidney"
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Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., TGgawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T.,
Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A.
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Institute of Mental Health (NIMH), Hemin Chin, Ph.D., program coordinator."	Alignment Scores: 2.9e-91 Length: 622 Pred. No.: 984.00 Matches: 180 Score: 984.00 Conservative: 0 Percent Similarity: 78.95* Mismatches: 2 Dest. Local Similarity: 78.95* Mismatches: 2	05.08* INCLES: 6 Gaps: 0-2 (1-275) x CB723138 (1-622)	Qy 1 MetGlyAlaProHisTrpTrpAspHisLeuArgalaGlySerSerGluValAspTrpCys 20	Oy 21 GluaspasnTyrThrIleValProAlaIleAlaGluBheTyrAsnThrIleSerAsnVal 40	Qy 41 LeuPhePhelleLeuProProlleCysMetCysLeuPheArgGlnTyrAlaThrCysPhe 60	Qy 61 AsnSerGly11eTyrLeu1leTrpThrLeuLeuValValValGly11eGlySerValTyr 80	Qy 81 PheHisAlaThrLeuSerPheLeuGlyGlnMetLeuAspGluLeuAlaIleLeuTrpVal 100	Oy 101 LeuMetCygAlaLeuAlaMetTrpPheProArgArgTyrLeuBroLysIlePheArgAsn 120	121 AspArgGlyArgPheLysAlaValValCygValLeuSerAlaileThrThrCysLeuAla 14	Db 436 GAC438 Oy 141 PhelleLysProAlalleAsnAsnIleSerLeuMetIleLeuGlyLeuProCysThrAla 160	438	Oy 161 LeuLeuValAlaGluLeuLysArgCysAspAsnValArgValPheLysLeuGlyLeuPhe 180	Oy 181 SerGlyLeuTrpTrpThrLeuAlaLeuPheCysTrpIleSerAspGlnAlaPheCysGlu 200	201	221 AlaSerTyrLeuGlyCysValCys 228	Db 598	54 S4 TION 6	ACCESSION BUJ32554 VPRSION BUJ32554.1 GI:25475352	SM
Db 309 TTCCATGCAACGCTGAGTTTCCTGGGTCAGATGCTTGATGAACTTGCCATTCTGTGGGTT 368 Qy 101 LeuMetCygAlaLeuAlaMetTrpPheProArgArgTyrLeuBroLygIlePheArgAsn 120	369 CHGATCHCHTHGGCCATGTCCCAGGAGTATTACCAAAGATCTTTCGGAAT 428 QY	Qy 141 PheIleLysProAlaIleAsnAsnIleSerLeuMetIleLeuGlyLeuProCysThrAla 160	Qy 161 LeuLeuValAlaGluLeuLysArgCysAspAsnValArgValPheLysLeuGly-LeuPh 180	Qy 180 eSerGlyLeuTrpThrLeuAla 188 bb 609 TTTGGCCTTGTGTGACTCTGGT 633	RESULT 12 CB723138 LOCUS LOCUS CB723138 CB723138 CB723138 CB723138 CB723138 CB723138 CB723138 CB720117171717171717171717171717171 MAD CHO Mis miscrilis CHA CANA CANA CANA CANA CANA CANA CANA	INAGE: 639525 5', mRNA sequence. CB723138.1 GI:29780280	KEYWORDS EST. SOURCE Mus musculus (house mouse) ORGANISM Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mu 1 (bases 1 to 622) NIH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC)	JOURNAL Unpublished (1999) COMMENT Contact: Robert Strausberg, Ph.D. Email: cgapbe-r@mail.nih.gov	Tissue Procurement: Dr. Jim Lin, University of Iowa CDNA Library preparation: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa			FEATURES LOCATION/QUALITIETB 1622 / organism="Mus musculus" / mol type="mRNA"	/strain="C57BL/6" /db_xref="taxon:10090" /clone="IMAGE:6839525" /+ione="IMAGE:A39525"	/dev_stage="1"5, and 15 days newborn" /dev_stage="1"5, and 15 days newborn" /lab_nost="nHTNB (TI phage resistant)" /lome lih="NHTN PARE GHO!"	/note="Organ: Brain; Vector: pXX- Asc; Site 1: BcoR I; Site 2: Not 1: The library was constructed according Site 2: Not 1: The library was constructed according to the part of the library was constructed according to the part of the library was constructed according to the part of the library was constructed according to the part of the library was constructed according to the part of the library was constructed according to the library was co	bonator, Lennon and Soares, Genome Research, 9:791-800, 1996. Denatured RNA was size fractionated on a 1% agarose gel. First strand CDNA synthesis was primed with oligo-dr primer containing a Not I site. Double strand CDNA was	<pre>size selected according to mkNA size fraction, ligated with EcoR I adaptor, digested with NotI and then cloned directionally into pYX-Asc vector. The library tag sequence located heaven the Not I site and the noled the column to the Not I site and the noled the column that the noled the nol</pre>	is CGAACTGAAT. This library was created for the University Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National

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CF169369 SAB bp mRNA linear EST 25-JUL-2003 B0812G07-5 NIA Mouse Newborn Kidney cDNA Library (Long 1) Mus musculus cDNA clone NIA:B0812G07 IMAGE:30468654 5', mRNA sequence.
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Piao,Y., Ko,N.T., Lim,M.K. and Ko,M.S.H.
Construction of long-transcript enriched cDNA libraries from submicrogram amounts of total RNAs by a universal PCR amplification
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  helysleuGlyLeuPheSerGlyLeuTrpTrpThrLeuAlaLeuPheCysTrp1leSerA
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ACAAAGCTTTTTGTGAGATCTGGTCATTTAACTTCCCCTATTTGCACTGTGTATGGC
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Laboratory of Genetics
National Institute on Aging/National Institutes of Health
133 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Email: cdna@Jgsun.grc.nia.nih.gov
Plate: B0812 row: G column: 07
Seg primer: M13 Reverse
High quality sequence stop: 548
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/db_xref="niaEG1:B0812G07"
/dov gtage="NRwborn Kidney"
/lab_host="DH10B"
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/ Jab host===012.9./
/ Jab host==01108"
/ Close==029an: heads, Vector: pBluescript II KS(+); Site_1:
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Scorstructed_from 1 million independent clones. CDNA
synthesis was initiated using an oligo(dT) primer, using
methylated C in the first strand reaction. Following this first strand reaction. Following this first strand reaction. Following this first of strand reaction. Following this first of strand reaction. Following this first of strand reaction. For the first strand reaction of the first strand reaction. For the first strand reaction was blunted, ligated to NotI adapters, digested with
ECORI, size-selected, and cloned into the NotI and ECORI
compatible sites of a custom modified MCS of the
pBluescript (KS4) vector. The library was normalized in 2
rounds using conditions adapted from Soares et al., PNAS
(1994) 91: 9228-9212 and Bonaldo et al., Genome Research 6
(1996): 791, except that a significantly longer
reannealing hybridization was used."
                                                                  Bosch, E.,
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                    Phasianinae; Gallus.

1 (bases 1 to 781)

Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J. A Comprehensive Collection of Chicken cDNAs

Curr. Biol. 12 (22), 1965-1969 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   76 IleGlySerValTyrPheHis-AlaThrLeuSerPheLeuGlyGlnMetLeuAspGluLe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 GGCTATICTCTGGGTCCTTATGTGTGCTTTGCCATGTGGTTCCCTAGGAGATATCTACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OLysllePheArgAsnAspArgGlyArgPheLysAlaValCysValLeuSerAlaIl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 ATTGGATCTGTTTACTTTCATGGCCACCTCAGCTTCCTGGGTCAGATGCTGGATGAGCT
                                                                                                                                                                                                                  Department of Biomolecular Sciences
University of Manchester Institute of Science and Technology
(UMIST)
Tel: 01612008930
Fax: 01612360409
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          781
177
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Gallus gallus"
/mol_type="mRNA"
/strain="White Leghorn, Hisex"
                                                                                                                                                                                                                                                                                                                                               Email: Simon.Hubbard@umist.ac.uk.
Location/Qualifiers
1. .781
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:9031"
/clone="ChEST323j2"
                                                                                                                                                                        12445392
Contact: Simon Hubbard
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JOURNAL
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                                                               AUTHORS
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purified by ethanol-precipitation. The cDNAs were ligated to Lone-linker LL-Sal4, purified by phenol/chloroform, and separated from free linkers by Centrion 100. Then, the CDNAs were amplified by long-range high fidelity PCR using Ex Taq polymerase (Takara) with a primer Sal4-S. The products were purified by phenol/chloroform and Centricon 100. The cDNAs were digested with Sal1 and Not1 enzymes and cloned into Sal1/Not1 site of pCMV-SPORT6 plasmid vector. The DH10B E. coli host was transformed with the ligation mixture by the standard chemical method. The average insert size is about 3.0 kb. The library was constructed by Yulan Piao."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TrpPheProArgArgTyrLeuProLysIlePheArgAsnAspArgGlyArgPheLysAla 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ValValCysValLeuSerAlaIleThrThrCysLeuAlaPheIleLysProAlaIleAsn 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABDIIESErLeuMetIIELeuGlyLeuProCygThrAlaLeuLeuValAlaGluLeuLyg 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 ATCTGCATGTGCTTCTTCCGCCAGTACGCACGTGCTTCAACAGCGGCATCTACTTAATA 180
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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78.95%
78.51%
60.85%
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Best Local Similarity:
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RESULT 15

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BJ060795 BJ060795 NIBB Mochii normalized Xenopus tailbud library Xenopus laevis cDNA clone XL066n16 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            163 ValAlaGluLeuLysArgCysAspAsnValArgValPheLysLeuGlyLeuPheSerGly 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LeuTrpTrpThrLeuAlaLeuPheCysTrpIleSerAspGlnAlaPheCysGluLeuLeu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    302 TITITGETGGACGCTGGCGTTGGCCTGTTGGATCAGTGACGAAGCTTTTTGTGAAATATGG 361
                                                                                                                    Eukaryota; Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Amphibia; Batrachia, Anura; Mesobatrachia, Pipoidea; Pipidae; Renopodinae; Xenopus.

( Dases 1 to 648)

( Kitayama, A., Terasaka, C., Mochii, M., Ueno, N., Shin-i, T. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61
                                                                                                                                                                                                                                                                                                                                                              is available through the following
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62 TCTGCGTTGGCCATGTGGTTCCCTAAAAGACACTTGCCAAGGGTATTTCGAAATGACAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    83 AlaThrLeuSerPheLeuGlyGlnMetLeuAspGluLeuAlaIleLeuTrpValLeuMet
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1. .648
|/organism="Xenopus laevis"
|/mol type="mRNA"
|/mol type="mRNA"
|/db xref="taxon:835s"
|/clone="XL066n16"
|/tissue_type="whole embryo"
|/dev_stage="stage_25"
|/clone_lib="NIBB Mochii normalized Xenopus tailbud
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              648
1162
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0
                                                                                                                                                                                                             Unpublished (2001)
Contact: Tadasu Shin-i
Contact: To Genetic Resource Information
Contact Institute of Genetics
Illi Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                            Xenopus laevis (African clawed frog)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps:
                                                                                                                                                                                                                                                                                                                                 Email: tshini@genes.nig.ac.jp
The information of this clone
URL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (1-648)
                                                                                                                                                                                                                                                                                                                                                                                         http://xenopus.nibb.ac.jp.
Location/Qualifiers
                                                BJ060795
BJ060795.1 GI:17500536
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908.00
93.78%
83.94%
60.05%
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Email: tshini@genes.
                                                                                                            Xenopus laevis
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Best Local Similarity:
Query Match:
                                                                                                                                                                                                       Kohara, Y.
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 LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No.:
                                                                                                           ORGANISM
                                           ACCESSION
VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                  TITLE
JOURNAL
COMMENT
                                                                                                                                                                        REFERENCE
                                                                                                                                                                                     AUTHORS
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AC097362 Rattus no CQ665547 Sequence AC109451 Homo sapi AL391834 Human DNA AR419744 Sequence BD115297 EST and e CQ615131 Sequence AC017406 Drosophil AC009365 Drosophil AC0093044 Drosophil AC0093044 Drosophil AC0093044 Drosophil AC0093044 Drosophil AC003044 Brosophil AC003104 Sequence AC017332 Drosophil CQ565546 Sequence AC017332 Drosophil CQ731034 Sequence AC1359502 Human DNA AL603886 Homo sapi CRE23187 Gallus ga CRE23187 Gallus ga G76816 S208P660FG BX664738 Zebrafish AC144710 Danio rer BX769176 Danio rer BX769176 Danio rer BX769176 Danio rer

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Isogai, T., Sugiyama, T., Otsuki, T., Wakamatsu, A., Sato, H., Ishii, S., Yamamoto, J., Isono, Y., Nagai, K. and Irie, R.
Full-length human cdna
Patent: EP 1440981-A 698 28-JUL-2004;
Research Association for Biotechnology (JP)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TTATTTTTCATTTTACCGCCCATCTGCATGTGCTTTGATGAGTATGCAACATGCTTG 180
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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17.4 219679
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11.5 187875
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ACCESSION
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ORGANISM
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AK206799 Sequence
AF282864 Mus muscu
BC059819 Mus muscu
CQ746905 Sequence
CQ736905 Sequence
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AF323976 Drosophil
AK10177 Ciona int
AL18206 Human DNA
AK116177 Ciona int
AK116177 Ciona spi
AK206797 Sequence
AF347024 Homo sapi
AK206797 Sequence
AF347024 Homo sapi
AK206797 Sequence
AF347024 Mus muscu
BX005084 Muse DNA
AC120245 Rattus no
                                                                                                      November 20, 2004, 20:50:21; Search time 3359.5 Seconds (without alignments) 11655.272 Million cell updates/sec
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            GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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construction: Helix Research Institute (HRI) (supported by Japan Rey Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: HRI and RAB; annotation: HRI and RAB.

Location/Qualifiers

1. 2852
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/clone lib="CTONG2"
/note="cloning vector: pMB18SFL3"
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Pred. No. 8.9e-210;
0; Mismatches 10;
                                                                                                                                      /organism="Homo sapiens"
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larity 98.8%;
Conservative (
                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 818; Conserv
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Direct Submission

Submitted (15-JUL-2003) Takao Isogai, FLJ Project (HRI Team); 2-6-7

Submitted (15-JUL-2003) Takao Isogai, FLJ Project (HRI Team); 2-6-7

Kazusa-Kamateari, Kisarau, Chiba 292-0818, Japan

(E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)

NEDO human CDNA sequencing project supported by Ministry of

Economy, Trade and Industry of Japan; CDNA full insert sequencing:

Research Association for Biotechnology (RAB); CDNA library
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oligo capping; fis (full insert sequence)
Homo sapiens (human)
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gai, T. and Yamamoto, J.
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398

458 360 518 420 578 480 638 540 698 009 758 999 818 720 878

(http://bacpac.med.buffalo.edu)

us-10-017-410-3.rge

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Submitted (09-JAN-2002) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA On Jan 9, 2002 this sequence version replaced gi:14165368.
                                                                                                                 PRI 09-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (09-DEC-1999) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 53108, USA 4 (bases 1 to 149462) Waterston, R.
                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mamaalia, Eutheria, Primates, Catarrhini, Hominidae, Homo. 1 (19462) Eulston, J.E. and Waterston, R.
                                                                                                               AC017081
Homo gapiens BAC clone RP11-470424 from 2, complete sequence
2 (bases 1 to 149462)
Nguyen,C., Doebber,A. and Kozlowicz,A.
The sequence of Homo sapiens BAC clone RP11-470J24
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                         sednence
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Genome Res. 8 (11), 1097-1108 (1998)
                                                                                                                                                                       AC017081.8 GI:18093316
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                                                                                                                                                                                                      Homo sapiens (human)
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Direct Submission
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VECTOR: PRACE3.6
NEIGHBORING SEQUENCE INFORMATION:
The clone sequenced to the left is RP11-310K15, 2000 bp overlap;
the clone sequenced to the right is RP11-156A1, 2000 bp overlap;
the clone sequenced to the sight is RP11-156A1, 2000 bp overlap.
Actual start of this clone is at base position 190775 of
RP11-310K15; actual end is at base position 28935 of RP11-156A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .771. .2127
'note="match to EST AW614820 (NID:97320006) hg80c08.x1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="match to EST AA054208 (NID:g1545131) zf51g03.rl"
                                                                                                                         The sequence between 81601 and 81703 is covered only by a pcr product of clone DNA. Unresolved tandem repeat regions exist between 81548 and 83183, 126196 and 127426.
Location/Qualifiers
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3207. .3758
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/rpt_family="AT_rich"
5518_.5847
//note="match to EST_R80994 (NID:g857275) yi94c08.rl"
5606..5633
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3486. .3527
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/note="match to EST AA056210 (NID:g1548612)
                                                                                                                                                                                                             /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /rpt_family="MER1_type"
2604. .2844
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2216. .2419
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5722. .5758
/rpt_family="AT_rich"
5802. .5831
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6965. .7000
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/rpt_family="MER1_type"
7982. .8006
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/rpt_family="(TGGG)n"
965. .1037
/rpt_family="GC_rich"
1127. .1561
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5808. .6116
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/rpt_family="AT_rich"
7020. .7094
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8000. .8436
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3501. .3745
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141. .282
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4231. .4273
                                                                                                                                                                                                                                                                                                       clone="RP11-470J24"
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/rpt_family="MIR"
2991. .3324
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/rpt_family="L2"
8437. .850^
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8541. 8696
/rpt_family="L2"
8722. 9684
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repeat_region

The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genemics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at the Roswell Park Cancer Institute

Louis

Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. I. MO. For additional information about the map position of this sequence, see http://genome.wustl.edu/gsc

MAPPING INFORMATION:

restriction digest.

SOURCE INFORMATION:

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by

NOTICE: This sequence may not represent the entire insert of this folore. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

Center: Washington University Genome Sequencing Center

Genome Center

COMMENT

Web site: http://genome.wustl.edu/gsc Contact: sapiens@watson.wustl.edu

Center code: WUGSC

Center project name: H_NH0470J24

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136801 TTATTTTCATTTTACGCCCCATCTGCATGTGCTTTTGTTTCGTCAGTATGCAACATGCTTC 136742
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                      CTGATGTGTGTGTTTTGGCCATGTGGTTCCCCAGAAGGTATCTACCAAAGATCTTTCGGAAT
                                                                                                181 AACAGTGACATCTACTTAATCTGGACTCTTTTGGTTGTAGTGGGAATTGGATCCGTCTAC
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Patent: WO 0155408-A 6 02-AUG-2001;
Memorec Medical Molecular Research Cologne Stoffel GmbH (DE)
Location/Qualifiers
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                                                                            Theses 1 to 4174)
Graveel, C.R., Jatkoe, T., Madore, S.J., Holt, A.L. and Farnham, P.J.
Identification of genes deregulated in murine hepatocellular
carcinomas using oligonucleotide microarrays and representational
                                                                                                                                                                          3. (Date: 10. 4174)

Farnham, P.J. and Graveel, C.R.

Farnham, P.J. and Graveel, C.R.

Fortham, P.J. and Graveel, C.R.

Submitted (27-UM-2000) Oncology, University of Wisconsin,
University Avenue, Madison, WI 53706, USA

Location/Qualifiers

1. 4174

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35. .862
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Oncogene 20 (21), 2704-2712 (2001)
                                                                                                                                                                                                                                                                                                                                                                           'note="CRG-L1; putative'
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Mismatches 30;
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ö 120 214 240 300 154 TIAITITITCAITITACCGCCCAICTGCAIGTGCTTGTTTGAIGAGTAIGCAACAIGCTTG 180 274 334 360 394 420 454 480 514 540 94 GAGGACAACTACACCATCGTGCTGCTATCGCCGAGTTCTACAACACGATCAGCAATGTC GAGGACAACTACACTATCGTGCCTGCCATTGCCGAGTTCTACAACACGATCAGGAACGTC TIGHTHITTCATTTTACCTCCCATCTGCATGTGCTTGTTCCGCCAGTACGCAACGTGCTTC AACAGCGGCATCTACTTAATATGGACGCTCCTAGTTGTAGTGGGGGATTGGATCTGTTAC Aredececececacresiesaceacerecesecrescastresacresaceresarresas AACAGTGACATCTACTTAATCTGGACTCTTTTGGTTGTAGTGGGAATTGGATCCGTCTAC TTCCATTTTACCCTTAGTTTCTTGGGTCAGATGCTTGATGAACTTGCAGTCCTTTGGGTT CIGCTCATCGCAGAGCTAAAGAGGTGTGACAACATGCGTGTGTTTAAGCTGGGCCTCTTC ATGGGCGCCCCGCACTGGGACCAGCTGCAGGCTGGTAGCTCGGAGGTGGACTGGTGC TTCCATGCAACGCTGAGTTTCCTGGGTCAGATGCTTGATGAACTTGCCATTCTGTGGGTT CTGATGTGTGCTTTTGGCCATGTGGTTCCCCAGAAGGTATCTACCAAAGATCTTTCGGAAT CTGATGTGTGTGTTTGGCCATGTGGTTTTCCCAGGAGGTATTTACCAAAGATCTTTCGGAAT GACAGGGGTAGGTTCAAGGTGGTCAGTGTCCTGTCTGCGGTTACGACGTGCCTGGCA 395 GACAGGGCAGGTTCAAGGCAGTGGTGTGTGTCTGTCTGCAATTACAACGTGCTTGGCG TITGTCAAGCCTGCCATCAACAACATCTCTGATGACCCTGGGAGTTCCTTGCACTGCA 455 TTTATCAAGCCCGCCATCAACAATATTTCCCTGATGATTCTGGGACTTCCATGCACTGCG Gaps . 4174; Length Score 664.8; DB 10; Length Pred. No. 1.1e-169; 0; Mismatches 102; Indels 421 481 d $\stackrel{\sim}{\circ}$ à

Mus musculus Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus. 1 (bases 1 to 4174) Graveel, C.R., Jatkoe, T., Madore, S.J., Holt, A.L. and Farnham, P.J.

REFERENCE AUTHORS

Mus musculus (house mouse)

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Klausner, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.L., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Schetz, T.E., Brownstein, M.J., Usdin, F., Casavant, T.L.,
Schetz, T.E., Brownstein, M.J., Usdin, T.E., Toshiyuki, S.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
MCKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,
Sanchez, A., Whitligg, M., Madan, A., Rodrigues, S.,
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Boutfard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Boutfard, G.G., Blakesley, R.W., Touchman, J.W., Schmutz, J., Myers, R.M.,
Generation and initial analysis of more than 15,000 full-length
Munan and mouse cDNA sequences
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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Submitted (07-COT-2003) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                 GCTGCCTACCTGGGCTGTGTATGCTTTTGCCTTTGATGCTGCCTCAGAGATTCCTGAG
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CTGCTTGTTGCAGAGCTGAAGAGGTGTGACAATGTGCGTGTGTTAAGCTGGGCCTCTTC
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. James Lin, University of Iowa
cDNA Library Preparation: M. Bento Soares, University of Iowa
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Genome Sequence Centre,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              #Mus musculus cancer related gene-liver 1, mRNA (cDNA clone MUSC 195283 IMAGE:6839525), complete cds.
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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 132 Row: o Column: 4
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 21314857.
Location/Qualifiers
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LPPETGMCLESYZATGNISTYLIWTLLIVVOGIGSVFFHATLALFERGGMDELALIWVLM
CALAMWFPRYLPRI FRUDRCDNYZVFKLGLFSGTAWTLALFCWISDQAFCELLSSFH
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                                                                                                Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield, Susama Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin, Letticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline Schein, Unane Smailus, Michael Smith, Lorraine Spence, Jeff Stott, Michael Thorne, Miranada Tsai, Natasia van den Bosch, Jill Vardy, George Yang, Scott Zuyderduyn, Marco Marra.
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/clone="MGC:69583 IMAGE:6839525"
/tissue_type="Barin"
/clone_lib="NIH_BMAP_GHO"
/lab_host="DH10B"
Vancouver, BC, Canada
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/protein id="AAH59819.1"
/db_xref="G1:37590520"
/db_xref="LocusID:230379"
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/strain="C57BL/6"
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420

361 GACAGGGGTAGGTTCAAGGTGGTGGTCAGTGTCTGTCTGCGGTTACGACGTGCCTGGCA

Qy 694 TTTGATGCTGCCTCAGAGATTCCTGAGGCCCTGTCATCAGTTCTGGCCCAATGAG 753 Db 181 TTTGATGCTGCCTCAGAGATTCCTGAGAGAGGCCTGTCATCAGTTCTGGCCCAATGAG 240 Qy 754 AAATGGGCCTTCATTGGTGTCCCTTGTGTGCCCTGTGTGCCAACAAGAAATCATCA 813 Db 241 AAATGGGCCTTCATTGGTGTCCCTTGTGTGCCTTCTGTGTGCCAACAAGAAATCATCA 300 Qy 814 GTCAAGATCACGTGA 828 Db 301 GTCAAGATCACGTGA 315		REFERENCE AUGUSTOCATOR TOTAL SUPPLIES ELECATOR TAMES TOTAL	/mol_type="unassigned DNA" /db_xref="taxon:9606" ORIGIN Query Match	Qy 574 TGGATCAGTGACCGAGCTTTCTGCGAGCTGCTGTCATCCTTCCACTTCCCTACCTGCAC 633 Db 61 TGGATCAGTGACCTTTCTGCGAGCTGCTGTCATCCTTCACTTCCCCTACCTGCAC 120 Qy 634 TGCATGTGGCATCTCTCTGCTGCTGCTACCTGGGCTGTATGCTTTGCCTAC 693 Db 121 TGCATGTGGCACATCCTCATCTGCCTTGCTGCTACCTGGGCTGTATGCTTTGCTAC 180 Qy 694 TTTGATGTGCTCTCACAGGCCTACTGCTACTGTATGTTTTGCTAC 180 Qy 694 TTTGATGTTGCTTCATGAGAGCCCTACTGTATGTATGCTACTACTACTACTACTACTACTACTACTACTACTACTAC		RESULT 9 CQ736906 LGCTS LGCTS LGCTS CQ736906 CQ736906 CQ736906 DEFINITION Sequence 22840 from Patent WO02068579. ACCESSION CQ736906 VERSION CQ736906.1 GI:42333767
	Db 478 TCTGGCCTCTGGTGGCTCTCTTCTGCTGGATCAGCGACCAAGCCTTCTGTGAG 537 Qy 601 CTGCTGTCATCCTTCAACTTCCCCTACCTGCATGAGCCATCTGCTGCATCTGCCGACCAACCTCTGCTGCGTT 660 Db 538 CTGCTCTCCTCTTCACTTCCCTACCTGCACTGTGTGGTGGCATATTCTCATCTGCCTT 597 Qy 661 GCTGCCTACCTGGGTGTATGCTTTGCTTTGATGCTTCATCTGAGATTCCTGAG 720 CD 661 GCTGCCTACCTGGGGTGTATGCCTTTGATGCTTTGATGCTTCATCTGAGATTCCTGAG 720 CD 661 GCTGCCTACCTGGGGTGTATGCTTTGCTTTGATGCTTCGAGAATTCCTGAG 720 CD 661 GCTGCCTACCTGGGGTGTATGCTTTGCTTTGATGCTTCGAGAATTCCTGAG 720	721 CAAGGCCTGTCATCAAGTTCTGGCCCAATGGAGAATGGGCCTTCATTGGTGTCCCC 721 CAAGGCCTGTCATCAAGTTCTGGCCCAATGGAGAATGGGCCTTCATTGGTGTCCCC 658 CAAGGTCCTGTGTGATTCTGGCCCAGAGAAATGGGCTTTTATTGTGTGTCCTT 781 GTGTCCTCCTGTGTGCCAACAAGAAATCATCAGAATCAGGTA 828	ITION Sequence 30030 from Patent W002068579. SION CQ744096 ON CQ744096.1 GI:42358801 RDS Homo sapiens (human) ANISM Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Butele Bukaryota; Primates; Catarrhini; Hominidae; Homo. ENCE 1 HORS Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W.	ALLE, SUCH AS INCIENT ALLE, SUCH AND AND AND AND AND AND AND AND AND AND	y Match Local Similarity 100.0%; Score 315; DB 6; Length 315; Local Similarity 100.0%; Pred. No. 1.5e-74; hes 315; Conservative 0; Mismatches 0; Indels 0; (514 ANGCGTGTGTTTAAGCTGGGCCTCTTCTCGGGCCTCTGGTGGACCTGGTGTTTAAGCTGGGCCTCTTCTCGGGCCTCTGGTGGACCTGGTGCCTGTTTAAGCTGGGGCCTTTCTGGGGCCTTTTGGGGCCTTGGTGGTGCCTGGTGCCTGGTGCCTGGTGCCTGGTGCTTCTGGGGCCTTTCTGGGGCCTGGTGCTTCTGGGGCCTTGGTGCTGC	Db 61 TGGATCAGTGCTTTTCTGGAGCTGCTTCTTTTTTTTTTT

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YLHGFWHIFFFIAAYTVLVLFAYFYVESELPQRQPLLKYWFKNFFEFGIPFISIRNPG
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llarity 57.6%; Pred. No. 5.1e-54;
Conservative 0; Mismatches 317;
                                                                                                                                        /protein_id="AAL55991.1"
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                                                                        /note="ceramidase; BWA"
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/gene="bwa"
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                           Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W.
Kits, such as nucleic acid arrays, comprising a majority of
humanexons or transcripts, for detecting expression and other
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/organism="Drosophila melanogaster"
/mol_type="mRNA"
/db_xref="taxon:7227"
/chromosome="2"
/map="38A"
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 308.6; DB 6;
Pred. No. 8.4e-73;
0; Mismatches 4;
                                                                                                                                                                                                                                  Patent: WO 02068579-A 22840 06-SEP-2002;
PE Corporation (NY) (US)

    .315
    /organism="Homo sapiens"
/mol_type="unassigned DNA"
    /db_xref="taxon:9606"

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Location/Qualifiers
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This clone was sequenced as part of a high-throughput process to sequence clones from Drosophila Gene Collection 1 (Rubin et al., Science 2000). The sequence has been subjected to integrity checks for sequence accuracy, presence of a polyA tail and contiguity within 100 kb in the genome. Thus we believe the sequence to reflect accurately this particular cDNA clone. However, there are artifacts associated with the generation of cDNA clones that may have not been detected in our initial analyses such as internal priming, priming from contaminating genomic DNA, retained introns due to reverse transcriptuse errors that result in single base changes. For further information about this sequence, including its location (http://fruitfly.berkely.edu) or send email to
                                                                                                                                                                                                                                             1 (bases 1 to 2318)
Stableton, M., Brokstein, P., Hong, L., Agbayani, A., Carlson, J.,
Champe, M., Chavez, C., Dorsett, V., Dresnek, D., Farfan, D., Frise, E.,
George, R., Gonzalez, M., Guarin, H., Kronmiller, B., Li, P., Liao, G.,
Miranda, A., Mungall, C.J., Nunco, J., Pacleb, J., Paragas, V., Park, S.,
Patel, S., Phouanenavong, S., Wan, K., Yu, C., Lewis, S.E., Rubin, G.M.
                                                INV 20-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /translation="MGGMGGGGLDIYAMAWEHLRPGSSPVDMCEGNYLISSNIAEFV
NTFSNFLFILLPPVLIMLFKEYGRFVTPGIHVINVLLIVVGLSSMYFHATLSLIGQLL
BEALLWYFWAAFSLFYPKYYPKFYWONDKTFSWIMLLSATAATGGGSWKPIVNAFV
LMFMSYPTWMLYTFELGNYSDQRVXRGIRSTTVWAVNFCWINDRTFCEAWSSINFP
YLHGFWHIFIFIAAYTVLVLFAAYFYVESELPQRQPLLKYWPKNEFEFGIPFISRNPG
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Low xref="FLYBASE:FBGN0032842"

404. .1255
                                                                                                                                                                 Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
Submitted (18-DEC-2001) Berkeley Drosophila Genome Project,
Lawrence Berkeley National Laboratory, One Cyclotron Road,
Berkeley, CA 94720, USA
Sequence submitted by:
Berkeley Drosophila Genome Project
Lawrence Berkeley, National Laboratory
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Drosophila melanogaster RE26924 full length cDNA.
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'organism="Drosophila melanogaster"
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Pred. No. 1.5e-53;
0; Mismatches 318;
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|db_xref="GI:17945606"
|db_xref="FLYBASE:FBGn0032842"
                                                                                                                                                Drosophila melanogaster (fruit fly)
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/strain="y; cn bw sp"
/db_xref="taxon:7227"
/map="3884-3885"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cdna@fruitfly.berkeley.edu.
Location/Qualifiers
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/note="Longest ORF"
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Best Local Similarity 57.4%;
Matches 429; Conservative (
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Ciona intestinalis
Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
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                Satou,Y. and Satoh,N.
Direct Submission
Submitted (04-OCT-2002) Nori Satoh, Kyoto University, Department
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                                                                  Zoology; Sakyo-ku, Kyoto, Kyoto 606-8502, Japan (E-mail:satohoascidian.zool.kyoto-u.ac.jp, Tel:81-75-753-4095, Fax:81-75-705-1113)
Ciona intestinalis CDNA Project (URL: http://ghost.zool.kyoto-u.ac.jp/indexr1.html).
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Pred. No. 1.1e-47;
0; Mismatches 329;
                                                                                                                                                                                      /organism="Ciona intestinalis"
                                                                                                                                                                                                        /mol_type="mRNA"
/db_xref="taxon:7719"
/clone="citb013n14"
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Direct Submission

Submitted (25-JUN-2000) Sanger Centre, Hinxton, Cambridgeshire, CENO 1834, UK. E-maile nequiries: hunquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk

On Jul 7, 2000 this sequence version replaced gi:8651879.

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure'
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Em.; EMBL; Sw.; SWISSPROT; Tr.; TREMBL; Wp.; WORWPEP; Information on the WORWPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 9, constructed by the Sanger Centre Chromosome 9 Mapping
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RP11-363E7 is from the library RPCI-11.2 constructed at the Roswell Park Cancer Institute by the group of Pieter de Jong. For further details see http://bacpac.med.buffalo.edu/
PRI 28-JUN-2000
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163542 bp DNA linear PRI 28-JUN-2000 sequence from clone RP11-363E7 on chromosome 9, complete
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 163542)
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/clone_lib="RPCI-11.2"
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97064 CTGCCTCAGAGATTCCTGAGGAAGGCCCTGTCATCAAGTTCTGGCCCAATGAGAAATGGG 97005
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/protein_id="AaL83822.1"
/db_xref="GI:19070367"
/translation="MPSIFAYQSSEVDWCESNFQYSELVAEFYNTFSNIPFFIFGPLM

    ..795
/function="deacylates ceramide to generate sphingosine and

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WARRCYFPSFLGGMSQPIRLVFITYWYSTLLSFRPTWAYALNSIALHIYYUCQB
YRKTSNYGLRHLIFSVYLMAYALTSWISDBLLCSFWQRIHFFYLHSIMHVLISITFP
YGMVTMALVDANYEMPGETLKVRYWPRDSWPVGLPYVBIRGDDFDC"
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Mao, C., Xu,R. and Obeid,L.M.
Molecular cloning and characterization of a novel human alkaline
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2 (bases 1 to 795)

Mao,C., Xu,R. and Obeid,L.M.
Direct Submission
Submitted (08-FEB-2001) Medicine, Medical University of South Carolina, 171 Ashley Avenue, Charleston, SC 29425, USA
                                                                                                                                                                                                            Length 219679;
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/clone="RP11-170C8"
/clone_lib="RPCI human BAC library 11"
                                                                                                                                                                                                       22.7%; Score 188; DB 2;
100.0%; Pred. No. 1e-39;
iive 0; Mismatches 0
                                           organism="Homo sapiens"
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                                                          /mol_type="genomic_DNA"
/db_xref="taxon:9606"
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/db_xref="taxon:9606"
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Consensus quality: 214895 bases at least Q30
Consensus quality: 216278 bases at least Q30
Consensus quality: 216278 bases at least Q30
Consensus quality: 216278 bases at least Q30
Consensus diality: 216278 bases at least Q30
Estimated insert size: 21000; agarcase-fp estimation
Quality coverage: 5.43 in Q20 bases; agarcase-fp estimation
(Quality coverage: 5.33 in Q20 bases; agarcase-fp estimation

* NOTE: This is a "working draft' sequence. It currently
consists of 9 contigs. The true order of the pieces

* is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will

* be preserved.
                                                                                                                                                                                                                           ACLU9451 219679 bp DNA linear HTG 04-FEB-2002 HOMO Sapiens chromosome 5 clone RP11-170C8, WORKING DRAFT SEQUENCE, 9 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
Submitted (04-FEB-2002) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
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1 (bases 1 to 219679)
DOB Joint Genome Institute.
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HTG; HTGS PHAKE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
HOMO sapiens (human)
HOMO sapiens
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Center Project Name: 471701
Center clone name: RPCI-11_170C8
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Center Code: JGI
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DOE Joint Genome Institute.
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PRI 02-MAR-2002

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Description	Abs54149 Human CDN	Accsusel Human Dla Adn38833 Cancer/an	Aah48641 Human cer	Abs54148 Mouse cDN	Adi21948 Novel hum	Ad106640 Human 3T3	Adl06642 Human 3T3	Adi21468 Novel hum	Aak51566 Human pol	Aak52550 Human pol	Aah48639 Human cer	Abl24043 Drosophil	Abl30432 Drosophil	Abl24042 Drosophil	Adc87616 Human GPC	Ada71938 Rice gene	Ada71938 Rice gene	Abx74425 Human cDN	Abl90053 Human pol	Aah07955 Human cDN
SUMMARIES	ABS54149	ACC50961 ADN38833	AAH48641	ABS54148	ADI21948	ADL06640	ADL06642	ADI21468	AAK51566	AAK52550	AAH48639	ABL24043	ABL30432	ABL24042	ADC87616	ADA71938	ADA71938	ABX74425	ABL90053	AAH07955
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ALIGNMENTS

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Novel polypeptide designated as CRG-L1, useful as diagnostic marker for liver cancer, is differentially expressed in liver tumors relative to normal liver tissues.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to a polypeptide designated as CRG-L1), which is differentially expressed in liver tumours relative to normal expression
                                                                                                                                                                                               /*tag= a
/product= "Liver tumour marker protein, CRG-L1"
                                                                                         Human cDNA encoding a liver tumour marker protein, CRG-L1.
                                                                                                              Human; 88; gene; liver cancer; liver tumour; CRG-Ll; hepatocellular cancer; chromosome 9p.
                                                                                                                                                                        Location/Qualifiers
                       ABS54149 standard; cDNA; 828 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 2; Page 8; 11pp; English.
                                                                                                                                                                                                                                                                             14-DEC-2001; 2001US-00017410.
                                                                                                                                                                                                                                                                                                     14-DEC-2000; 2000US-0255674P.
                                                                   (first entry)
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                                                                                                                                                   Homo sapiens.
                                                                  25-NOV-2002
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                                            ABS54149;
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RESULT 1
          ABS54149
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                                                                                                                                                                                                                                                                                                                                    9
               encoding polynucleotides (in the case of the human sequence, mapping to chromosome 9p), expression constructs, host cells, anti-CRG-L1 antibodies, identifying modulators of CRG-L1, and the use of the CRG-L1 sequence in the diagnosis of hepatocellular cancer in tumour cells from liver of a human or non-human animal. The CRG-L1 protein and polynucleotide are useful as diagnostic markers for a liver cancer in humans and non-human animals, and as a system for assessing putative therapeutic agents. The present sequence encodes human CRG-L1
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 designated CRG-L1. Also included are the
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                                                                                                                                                                                                                           Length 828;
                                                                                                                                                                                      Sequence 828 BP; 157 A; 216 C; 211 G; 244 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                       100.0%; Score 828; DB 6; L 100.0%; Pred. No. 5.7e-242;
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normal liver tissues,
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Best Local Similarity
Matches 828; Conserv
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The present invention describes a method for detecting a bladder cancerassociated transcript in a cell from a patient. The method comprises contacting a biological sample from the patient with a polynucleotide that selectively hybridises to a sequence that is 80 % identical to a table of sequences (see ACC5051 to ACC51059). ACC5051 to ACC51059 encode the human bladder cancer-associated proteins given in ABR48146 to have cytostatic activities, and can be used in antisense gene therapy and in vaccine production. The method can be used for detecting a bladder cancer-associated and used for detecting a bladder cancer-associated transcript in a cell from a patient. The method is useful in diagnosting or treating bladder cancer and in screening for compounds that modulate bladder cancer, such as hormones or antibodies. The nucleic acid molecules from the present invention may be used in various screening and diagnostic methods, and for gene therapy, vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATGGGGCCCCGCACTGGTGGGACCAGCTGCAGGCTGGTAGCTCGGAGGTGGACTGGTGC 136
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patient v
                                                                                                                                                                                 88
                                                                                                                                                                               Human; bladder cancer; cytostatic; gene therapy; vaccine; gene;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Detecting a bladder cancer-associated transcript in a cell patient, comprises contacting a biological sample from the bladder cancer-associated polynucleotide or antibody.
                                                                                                                                           Human bladder cancer associated cDNA sequence SEQ ID NO:21.
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Pred. No. 3.4e-237;
0; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and/or antisense/inhibition applications
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 6; Page 235; 307pp; English.
                                   BP.
                                   ACC50961 standard; cDNA; 4202
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03-AUG-2001; 2001US-0310099P.
08-NOV-2001; 2001US-0343705P.
13-NOV-2001; 2001US-0350666P.
12-APR-2002; 2002US-0372246P.
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Best Local Similarity 98.9
Matches 819; Conservative
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                                                                                                                                                                                                                     Homo sapiens.
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                                                                       ACC50961;
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            AACAGTGGCATCTACTTAATCTGGACTCTTTTGGTTGTAGTGGGAATTGGATCCGTCTAC
                                      TICCATITIACCCTIAGITICIAGGICAGAIGCTIGAIGAACAIGCAGICCTITGGGII
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AACAGTGACATCTACTTAATCTGGACTCTTTTGGTTGTAGTGGGAATTGGATCCGTCTAC
                                                   CTGATGTGTGCTTTGGCCATGTGGTTCCCCAGAAGGTATCTACCAAAGATCTTTCGGAAT
                                                                                                                                           GACCGGGGTAGGTTCAAGGTGGTCAGTGTCCTGTCTGCGGTTACGACGTGCCTGGCA
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                                                                                                   CTGATGTGTGCTTTTGGCCATGTGGTTCCCCAGAGGTATCTACCAAAGATCTTTCGGAAT
                                                                                                                      GACAGGGTAGGTTCAAGGTGGTCAGTGTCCTGTCTGCGGTTACGACGTGCCTGGCA
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21-NOV-2001; 2001US-0332464P.
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The invention relates to nucleic acids and proteins (ADN38683-ADN40064)
whose expression is upregulated or downregulated in specific cancers or
context diseases such as angiogenic or fibrotic disorders, and to methods
of determining the presence or absence of a pathological cell in a
confering a nucleic acid at least 80% identical to those of
the invention or by detecting a polypeptide of the invention. The
invention also relates to expression vectors and host cells comprising a
concleic acid of the invention; antibodies which specifically bind a
polypeptide of the invention; antibodies which specifically bind a
colypeptide of the invention; use of such antibodies for drug targeting;
cond methods of screening for modulators of activity or expression of the
polypeptides and nucleic acids. The nucleic acids, polypeptides,
antibodies and methods are useful for diagnosing, prognosing and treating
cancer and other conditions such as psoriasis, ischaemia, heart disease,
atherosclerosis, inflammatory diseases, autoimmune diseases, retinal
cneovascularistaion syndromes, scarring and uterine fibroids. They may
also be useful in wound healing and in contraception. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Determining the presence or absence of a pathological cell in a patient, useful for diagnosing, prognosing or treating cancer, comprises detecting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TICCATTITACCCTIAGITICTIGGGICAGAIGCTIGAAGAACTIGCAGICCTITGGGTT 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gish KC, Glynne R, Hevezi PA;
Wilson KE, Zlotnik A;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 8; SEQ ID NO 151; 1385pp; English.
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                          2001US-0335394P.
2001US-0340376P.
2002US-0347211P.
2002US-0357349P.
2002US-0355250P.
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2002US-0368809P.
2002US-0370110P.
2002US-0372246P.
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13-FEB-2002; 2
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29-NOV-2001;
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14-DEC-2001;
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This invention describes novel human ceramidase (I) containing a specific structural motif which has antiproliferative, anticancer, anti-eczema, antipsoriasis and dermatological activity. (I) cleave ceramide, resulting in formation of sphingosine. (I), or the nucleic acid (II) encoding it, are used for diagnosis, prevention or treatment of diseases associated with ceramide defects, particularly altered cell proliferation (cancer) or altered ceramide layers on the skin (neurodermatitis, eczema, psoriasis), also for targeted modification of the permeability barrier by ceramidase or its activators, e.g. for transcutaneous delivery of substances. Specifically they are used for diagnosis of ichthyosis, This sequence encodes human ceramidase K3
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of ceramidase defects, e.g.
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diagnosis, prevention and treat
ichthyosis, also in cosmetics.
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Best Local Similarity
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/transl_except= (pos:382. .387,aa:Cys)
/note= "No stop codon given"
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  1 ATGGCCCCCCCCCCCCTGGTGGACCAGCTGCAGCTGGTAGCTCGGAGGTGGACTGGTGC
                                                                                                 GAGGACAACTACACCATCGTGCCTGCTATCGCCGAGTTCTACAACACGATCAGCAATGTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel polypeptide designated as CRG-L1, useful as diagnostic marker for liver cancer, is differentially expressed in liver tumors relative to normal liver tissues.
GCTGCCTACCTGGGCTGTGTATGCTTTGCCTACTTTGATGCTGCCTCAGAGATTCCTGAG
                         GCTGCCTACCTGGGCTGTGTATGCCTACTTTGATGCTGCCTCAGAGATTCCTGAG
                                                                                                                           CAAGGCCCTGTCATCAAATTCTGGCCCCAGGGAAATGGGCCTTCATTGGTGTCCCCTAT
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/product= "Liver tumour marker protein, CRG-L1"
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80.3%; Score 664.8; DB 6; Length 4175;
Best Local Similarity 87.7%; Pred. No. 9.5e-192;
Matches 726; Conservative 0; Mismatches 102; Indels 0;
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                                                                                                                                                                                         GTGTCCCTCCTGTGTGCCAACAAGAATCATCAGTCAAGATCACG 825
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mouse cDNA encoding a liver tumour marker protein, CRG-L1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gene; liver cancer; liver tumour; CRG-L1;
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                                                                                                                                                                                                                                                                                                                                                       ABS54148 standard; cDNA; 4175
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P-PSDB; ABG32880.
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forensic; nutritional source; damaged tissue; diseased tissue; myeloid cell disorder; lymphoid cell disorder; bone cartilage tissue growth; tendon tissue growth; ligament tissue growth; nerve tissue growth; regeneration; wound healing; tissue repair; tissue replacement; burn; incision; ulcer; cancer; human;
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ADI21948 standard; cDNA; 1623
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This invention describes a novel human protein with 3T3 cell conversion promoting function, polynucleotides encoding the polypeptide and the recombinant process of producing the polypeptide. The present invention also discloses the agonist resisting the polypeptide and its treatment effect. The present invention also discloses the application of the polynucleotides encoding the human protein with 3T3 cell conversion
                                                              1280 TGCTTTGCCTACTTTGATGCTGCCTCAGAGATTCCTGAGGGCCAAGGTCATCATGAGTTC
                                                                                                                      TGGCCCAATGAGAATGGGCCTTCATTGGTGTCCCCTATGTGTCCCTCCTGTGTGCCAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GATCAGCAATGTCTTATTTTCATTTTACCGCCCATCTGCATGTGCTTTGATGAGTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein with function of promoting 3T3 cell conversion and its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1527;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3; DB 10;
1.3e-115;
hes 17; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (SHAN-) SHANGHAI XINSHIJIE GENE TECHN DEV CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human 3T3 cell conversion promoter PP11646 cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3T3 cell conversion; promoter; human; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 414.8; E
Pred. No. 1.3e-
0; Mismatches
                                                                                                                                                                                                                           AAGAAATCATCAGTCAAGATCACGTGA 828
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 1; SEQ ID NO 1; 41pp; Chinese.
                                                                                                                                                                                                                                                                                                                                         ADL06640 standard; cDNA; 1527 BP
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82.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to an isolated polynucleotide encoding a polypeptide with biological activity. The polynucleotides and polypeptides are useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders and other traits, to assess biodiversity, as nutritional sources or supplements. The polynucleotides may also be used as mulecular weight markers, chromosome markers or map related gene positions, or as an antigen to raise anti-DNA antibodies or elicit immune response. The polypeptides are useful for raising antibodies, as markers for tissues in which the corresponding polypeptide is expressed, for re-engineering damaged or diseased tissues, for treating myeloid or lymphoid cell disorders, in bone cartilage, tendon, ligament and/or nerve tissue growth or regeneration, in wound healing, in tissue repair and replacement, in healing of burns, incisions and ulcers, and in treating cancer. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              681
                                                                                                                                                                                                                                                                                                                                                                                                                                         New polynucleotides and secreted proteins, useful for treating myeloid or lymphoid cell disorders, in bone cartilage, tendon, ligament and nerve tissue growth or regeneration, in wound healing, and in tissue repair and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGGTTCCCCAGAAGGTATCTACCAAAGATCTTTCGGAATGACAGGGGTAGGTTCAAGGTG 381
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                                                                                                                                                                                                                                                                                                    Wang J;
Wang D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CCCTACCTGCACTGCATGTGGCACATCTCCTCCTTGCTGCTGCCTACCTGGGCTGTGTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GCCCTGTTCTGCTGGATCAGTGACCGAGCTTTCTGCGAGCTGCTGTCATCCTTCAACTTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequence represents cDNA encoding a novel human protein.
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                                                                                                                                                                                                                                                                                         Tang YT, Asundi V, Goodrich RW, Ren F, Zhang J, Zhao QA,
Ghosh M, Xue AJ, Wehrman T, Weng G, Zhou P, Drmanac RT,
Haley-Vicente D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1623 BP; 305 A; 457 C; 382 G; 479 T; 0 U; 0 Other;
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                       GATCTTTCGGAATGACAGGGTAGGTTCAAGGTGGTGGTCAGTGTCTGCGGGTTAC
                                                                                                                 TCCTTGCACTGCACTGCTCATCGCAGAGCTAAAGAGGCATGAGGAACCAGCGAAGGAG
                                                                                                                                                AGTCCTTTGGGTTCTGATGTGTGCTTTGGCCATGTGGTTCCCCAGAAGGTATCTACCAAA
                                                                       GACGTGCCTGGCATTTGTCAAGCCTGCCATCAACAACATCTCTGATGACCTGGGAGT
                                                                                                                                                                        GACCCCGTGCAGGTGTGACAACATGCGTGTGTTTTAAGCTGGGCCTCTTCTCGGGCCTCT
                                                                                                                                                                                           GGTGGACCCTGCCCTGTTCTGCTGGATCAGTGACCGAGCTTTCTGCGAGCTGCTGTCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  promoting 3T3 cell conversion and
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                                                                                                                                                                                                                       CCTTCAACTTCCCCTACCTGCACTGCATGTGGCACATCCTCATCTG 656
                                                                                                     TCCTTGCACTGCACTGCTCATCGCAGAGCTAAAG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                              (SHAN-) SHANGHAI XINSHIJIE GENE TECHN DEV CO LTD.
                                                                                                                                                                                                                                                                                                                     Human 3T3 cell conversion promoter PP11646 DNA
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/product= "PP11646"
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This invention describes a novel human protein with 3T3 cell conversion promoting function, polymuclectides encoding the polypeptide and the recombinant process of producing the polypeptide. The present invention also discloses the agonist resisting the polypeptide and its treatment effect. The present invention also discloses the application of the polymuclectides encoding the human protein with 3T3 cell conversion
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1527 BP; 376 A; 357 C; 383 G; 411 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CCTTCAACTTCCCCTACCTGCACTGCATGTGGCACATCCTCATCTG 656
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       50.1%; Score 414.8; DB 10; Length 82.4%; Pred. No. 1.3e-115; live 0; Mismatches 17; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ilarity 82.4%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          180
                                                                                                                                                                                                                                                                                                                                                  New polynucleotides and secreted proteins, useful for treating myeloid or lymphoid cell disorders, in bone cartilage, tendon, ligament and nerve tissue growth or regeneration, in wound healing, and in tissue repair and
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ligament tissue growth; nerve tissue growth; regeneration; wound healing; tissue repair; tissue replacement; burn; incision; ulcer; cancer; human; ss; gene; EST; expressed sequence tag.
                                                                                                                                                                                                                                                   Wang J;
Wang D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       159 ATGGGCGCCCCGCACTGGTGGGACCAGCTGCAGGCTGGTAGCTCGGAGGTGGACTGGTGC
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                                                                                                                                                                                                                                       Tang YT, Asundi V, Goodrich RW, Ren F, Zhang J, Zhao QA,
Ghosh M, Xue AJ, Wehrman T, Weng G, Zhou P, Drmanac RT,
Haley-Vicente D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 37.8%; Score 313; DB 10; Length 487; Best Local Similarity 97.0%; Pred. No. 8.5e-85; Matches 319; Conservative 0; Mismatches 10; Indels C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 487 BP; 81 A; 138 C; 131 G; 134 T; 0 U; 3 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                           Example 2; SEQ ID NO 719; 156pp; English
                                                                                                                                                   19-SEP-2002; 2002WO-US029964
                                                                                                                                                                            19-SEP-2001; 2001US-0323739P.
13-SEP-2002; 2002US-00323739
                                                                                                                                                                                                                                                                                                           WPI; 2003-354603/33.
                                                                                                                                                                                                                        (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                          P-PSDB; ADI21688
                                                                                          WO2003025148-A2
                                                               Homo sapiens.
                                                                                                                      27-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                replacement
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The invention relates to polymucleotides (AAK51456-AAK53435) and the encoded polygeptides (AAM78323-AAM80302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polymoleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. steem cell growth factor activity, immunomodulatory activity and activity, tissue growth factor activity, immunomodulatory activity and activin/inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leuxeamma, nervous system disorders, arthritis and inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the sequence listing were missing at the time of publication
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic acids encoding polypeptides with cytokine-like activities, useful
in diagnosis and gene therapy,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopolesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorder; arthritis; inflammation; ss.
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Chen R, Wang ZW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches 360; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drmanac RT, Asundi V, Zhou P, Xv
Wang D, Wang J, Zhang J, Ren F,
Wejhrman T, Goodrich R;
                                          459 CTGATGTGTGTTTAGCCATGTGGTTCCC 487
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Ma Y, Zhao QA, Wang D, Wang
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The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to cytokine, call proliferation or call differentiation or which may induce production of other cytokines in other call populations. The polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, immunomodulatory activity and activity tissue growth factor activity, immunomodulatory activity and activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111
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03-FEB-2000; 2000US-00496914.
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20-UDN-2000; 2000US-00598075.
19-ULL-2000; 2000US-0063925.
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                                                                           0 Other;
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                                                                           C; 200 G; 206 T; 0 U;
                                                                                                                                                                            0, Mismatches 356;
                                                                                                                             Score 183.4; DB 4;
                                                                                                                                                       Pred. No. 4.2e-45
  ΞĦ
particularly lamellar ichthyosis ICR2. This sequence encodes human ceramidase
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53.3%;
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                                                                                                                                                                                                                                                                                                                              TGGCATGTGCTCATCAGCATCACCTTCCCTTATGGCATGGTCACCATGGCCTTGGTGGAT 739
                                                                                                                                                                                                                                                                                                                                                                               GCTGCCTCAGAGATTCCTGAGCAAGGCCCTGTCATCAAGTTCTGGCCCAATGAGAAATGG 759
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ceramidase; human; K1; antiproliferative; anticancer; anti-eczema; antipsoriasis; dermatological; ceramide; sphingosine; treatment; ds; altered cell proliferation; cancer; neurodermatitis; eczema; cosmetic; permeability barrier; psoriasis; ichthyosis; lamellar ichthyosis ICR2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               760 GCCTTCATTGGTGTCCCCTATGTGTCCCTCTGTGTGCCAACAAGAAATCATCAGTC 816
  AGTGACCGAGCTTTCTGCGAGCTGCTGTCATCCTTCAACTTCCCCTACCTGCACTGCATG
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                                                                                                                                                                                                                                                                                                     The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB573737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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0; Mismatches 212; Indels
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genes from Drosophila and for elucidating ce
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila melanogaster genomic polynucleotide SEQ ID NO 42769.
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61.0%; Pred. No. 6.6e-18;
tive 0; Mismatches 99;
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11-JUL-2000; 2000US-00614150.
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pharmaceutical; gene; ds.
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Best Local Similarity
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3404 ACTICTACGIGGAAICGGAGCIGCCCCAGCGACAGCCGCIGCIGAAGIACIGGCCAAAGA 3463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   108 GATCAGCAAIGTCTTATTTTTCATTTTACCGCCCATCTGCATGTGCTTTGATGAGTA 167
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pharmaceutical; gene; ds.
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Best Local Similarity 55.6%; Pred. No. 1.4e-11;
Matches 144; Conservative 0; Mismatches 115; Indels
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11-JUL-2000; 2000US-00614150.
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                                 752 AGAAATGGGCCTTC
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228 TGGATCCGTCTACTTCCATTTTACCCTTAGTTTCTTGGGTCAGATGCTTGATGAACTTGC

288 AGTCCTTTGGGTTCTGATGTGTGTTTTGGCCATGTGGTTCCCCAGAAGGTATCTACCAAA 347

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Db 3467 CAIACTCTGGGTCTTTTGGCTCTTTTTGGTCTCTATCCGAGGGTACTATCCCAA 3526

Oy 348 GATCTTTCGGAATGACAGG 366

Db 3527 GTTCGTGAAAAACGATCGG 3545

Search completed: November 20, 2004, 21:28:48

Job time : 355:193 secs
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TYPE: DNA
ORGANISM: Homo sapiens
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ZIP: 22313-0299
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US-09-621-976-11241/c
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LENGTH: 358
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1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
             GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-08-232-463-14
US-09-07-005-17
US-09-244-796-17
US-09-144-394-3
US-09-489-039A-106
US-09-489-039A-106
US-09-475-515-68
US-09-475-515-65
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US-09-621-976-15639
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US-08-480-751-1
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US-08-484-719B-1
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US-08-164-839-30
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Maximum Match 100%
Listing first 45 summaries
                                                                     - nucleic search, using sw model
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                                                                    Sequence
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APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Larchner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
STATE: VA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-621-976-18033
US-08-164-839-32
US-08-583-799-30
US-08-583-799-32
US-08-164-839-69
US-08-164-839-71
US-08-164-839-71
US-08-33-799-69
US-08-314-309A-1
US-09-131-118-1
US-09-161-443-1
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US-09-103-840A-1
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          4.1 2064 1 2064 1 2064 1 2064 1 2064 1 2048 1 2048 1 2048 1 2048 1 2048 1 2048 1 2006 3 4.1 2007 3 4.1 2067 3 4.1 2067 3 4.1 2067 3 4.1 2067 3 4.1 2067 3 4.1 2067 3 4.1 2067 3 4.1 2067 3 4.1 2067 3 4.1 2067 3 4.1 2067 3 4.1 2067 3 4.1 2067 3 4.1 2067 3 4.1 2067 3 4.1 2067 3 4.1 2067 3 4.1 2067 3 4.1 2067 3 4.1 2067 3 4.1 2067 3 4.1 2067 3 4.1 2067 3 4.1 2067 3 4.1 2067 3 4.1 2067 3 4.1 2067 3 4.1 2067 3 4.1 2067 3 4.1 2067 3 4.1 2067 3 4.1 2067 3 4.1 2067 3 4.1 2067 3 4.1 2067 3 4.1 2067 3 4.1 2067 3 4.1 2067 3 4.1 2067 3 4.1 2067 3 4.1 2067 3 4.1 2067 3 4.1 2067 3 4.1 2067 3 4.1 2067 3 4.1 2067 3 4.1 2067 3 4.1 2067 3 4.1 2067 3 4.1 2067 3 4.1 2067 3 4.1 2067 3 4.1 2067 3 4.1 2067 3 4.1 2067 3 4.1 2067 3 4.1 2067 3 4.1 2067 3 4.1 2067 3 4.1 2067 3 4.1 2067 3 4.1 2067 3 4.1 2067 3 4.1 2067 3 4.1 2067 3 4.1 2067 3 4.1 2067 3 4.1 2067 3 4.1 2067 3 4.1 2067 3 4.1 2067 3 4.1 2067 3 4.1 2067 3 4.1 2067 3 4.1 2067 3 4.1 2067 3 4.1 2067 3 4.1 2067 3 4.1 2067 3 4.1 2067 3 4.1 2067 3 4.1 2067 3 4.1 2067 3 4.1 2067 3 4.1 2067 3 4.1 2067 3 4.1 2067 3 4.1 2067 3 4.1 2067 3 4.1 2067 3 4.1 2067 3 4.1 2067 3 4.1 2067 3 4.1 2067 3 4.1 2067 3 4.1 2067 3 4.1 2067 3 4.1 2067 3 4.1 2067 3 4.1 2067 3 4.1 2067 3 4.1 2067 3 4.1 2067 3 4.1 2067 3 4.1 2067 3 4.1 2067 3 4.1 2067 3 4.1 2067 3 4.1 2067 3 4.1 2067 3 4.1 2067 3 4.1 2067 3 4.1 2067 3 4.1 2067 3 4.1 2067 3 4.1 2067 3 4.1 2067 3 4.1 2067 3 4.1 2067 3 4.1 2067 3 4.1 2067 3 4.1 2067 3 4.1 2067 3 4.1 2067 3 4.1 2067 3 4.1 2067 3 4.1 2067 3 4.1 2067 3 4.1 2067 3 4.1 2067 3 4.1 2067 3 4.1 2067 3 4.1 2067 3 4.1 2067 3 4.1 2067 3 4.1 2067 3 4.1 2067 3 4.1 2067 3 4.1 2067 3 4.1 2067 3 4.1 2067 3 4.1 2067 3 4.1 2067 3 4.1 2067 3 4.1 2067 3 4.1 2067 3 4.1 2067 3 4.1 2067 3 4.1 2067 3 4.1 2067 3 4.1 2067 3 4.1 2067 3 4.1 2067 3 4.1 2067 3 4.1 2067 3 4.1 2067 3 4.1 2067 3 4.1 2067 3 4.1 2067 3 4.1 2067 3 4.1 2067 3 4.1 2067 3 4.1 2067 3 4.1 2067 3 4.1 2067 3 4.1 2067 3 4.1 2067 3 4.1 2067 3 4.1 2067 3 4.1 2067 3 4.1 2067 3 4.1 2067 3 4.1 2067 3 4.1 2067 3 4.1 2067 3 4.1 2067 3 4.1 2067 3 
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Best Local Similarity 99.1
Matches 109; Conservative
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       369 TAGGTTCAAGGTGGTCAGTGTCTGTCTGCGGTTACGACGTGCCTGGCATTTGTCAA 428
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        669 CCTGGGCTGTGTATGCTTTGCCTACTTTGATGCTGCCTCAGAGATTCCTGAGGCAAGGCCC 728
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0
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COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPDY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
GURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
                                                                                                                    PILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE:
FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMMU
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRAN: (703)836-9300
                                                                                                                                                                                                                                                                                                                                                                  TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
'PMCTH: 7218 base pairs
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TYPE: nucleic acid
STRANDEDNESS: single
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US-08-232-463-14
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RESULT 3 US-09-007-005-17/c ; Sequence 17, Application US/09007005B ; Patent No. 6258558

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507 TGACAACATGCGTGTGTTTAAGCTGGGCCTCTTCTCGGGCCTCTGGTGGACCCTGGCCCT 566
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                                              AFPLICANT: Liu, Rihe
TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN
TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN
TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN
FILE REFERENCE: 07986/350003
CURRENT APPLICATION NUMBER: US/09/007,005B
CURRENT FILING DATE: 1998-01-14
EARLIER FILING DATE: 1997-01-27
RARLIER FILING DATE: 1997-01-27
RARLIER FILING DATE: 1997-11-06
NUMBER OF SEQ ID NOS: 33
SOFTWARE: FRASEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 17, Application US/09244796

| Sequence 17, Application US/09244796
| Patent No 6281344
| GENERAL INFORMATION:
| APPLICANT: Scottak, Jack W. |
| APPLICANT: Liu, Rihe
| TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN
| TITLE OF INVENTION: FUSIONS |
| FILE REFERENCE: 00786/350007 |
| CURRENT APPLICATION NUMBER: US/09/244,796 |
| CURRENT APPLICATION NUMBER: 00/035,963 |
| EARLIER FILING DATE: 1997-01-27 |
| BARLIER FILING DATE: 1997-11-06 |
| BARLIER FILING DATE: 1997-11-06 |
| BARLIER FILING DATE: 1997-11-06 |
| BARLIER FILING DATE: 1997-01-36 |
| BARLIER FILING DATE: 1997-01-46 |
| NUMBER OF SEQ ID NOS: 33 |
| NUMBER OF SEQ ID NOS: 33 |
| SOFTWARE: FaetSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc_feature
i_LOCATION: (1)...(289)
/ OTHER INFORMATION: n = A,T,C or G
US-09-007-005-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: RNA
ORGANISM: Artificial Sequence
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APPLICANT: Szostak, Jack W.
APPLICANT: Roberts, Richard W.
                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 17
LENGTH: 289
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LENGTH: 289
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                                                                                                                                                                                                                                                    567 GITCTGCTGGATCAGTGACCGAGCTTTCTGCGAGCTGCTGTCATCCTTCAACTTCCCCTA 626
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4.9%; Score 40.2; DB 4; Length 1063;
Best Local Similarity 57.6%; Pred. No. 0.035;
Matches 72; Conservative 0; Mismatches 53; Indels 0
                                                                                                                   4.9%; Score 40.8; DB 3; Length 289; 6.9%; Pred. No. 0.011; tive 95; Mismatches 106; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: No. 6783969el Nucleic Acids and TITLE OF INVENTION: Polypeptides FILE REFERENCE: 803
                                                                                                                                                                                                                                                                                                                                                                                         687 IGCCIACTITGAIGCIGCCICAGAGAIICCIGAGCA 722
                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/799,451
CURRENT FILING DATE: 2011-03-05
NUMBER OF SEQ ID NOS: 948
SOFTWARE: DL_FL_genee Version 2.0
OTHER INFORMATION: Translation template FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 875, Application US/09799451
Patent No. 6783969
                               ; NAME/KEY: misc_feature
; LOCATION: (1)...(289)
; OTHER INFORMATION: n = A,T,C or G
US-09-244-796-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Zhang, Jie
Xue, Aidong J.
Zhao, Qing A.
Wang, Jian-Rui
Ma, Yunqing
Yamazaki, Victoria
Chen, Rui-hong
Wang, Zhiwei
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Drmanac, Radoje T.
                                                                                                                 Query Match
Best Local Similarity 6.9%;
Matches 15; Conservative
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Goodrich, Ryle
Asundi, Vinod
Ren, Feiyan
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; NAME/KEY: CDS
; LOCATION: (2)..(802)
US-09-799-451-875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
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LENGTH: 1063
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APPLICANT:
APPLICANT:
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APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PREUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Fink, Michel
APPLICANT: Fink, Michel
APPLICANT: Fink, Michel
APPLICANT: Lazdunski, Michel
TITLE OF INVENTION: FAMILY OF MAMMALIAN POTASSIUM CHANNELS, THEIR CLONING
TITLE OF INVENTION: AND THEIR USE, ESPECIALLY FOR THE SCREENING OF DRUGS
FILE REFERENCE: 989.6705CIP
CURRENT APPLICATION NUMBER: US/09/144,914
CURRENT APPLICATION NUMBER: 08/749,816
BARLIER APPLICATION NUMBER: 08/749,816
BARLIER FILLING DATE: 1998-08-04
BARLIER FILLING DATE: 1998-08-04
BARLIER PILLING DATE: 1998-08-04
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BARLIER PILLING DATE: 1998-08-04
BARLIER PILLING DATE: 1998-08-04
BARLIER PILLING DATE: 1998-08-04
SOFTWARE: PATENTING VALVE CO.2.0
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71 AACTACTCCGTGACCTGGTACATCGCCGAGTTCTGGAATACAGTGAGTAACCTGATCATC 130
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                                                                                                                                                                                                                                                                                                      Sequence 3, Application US/09144914
Patent No. 6309855
GENERAL INFORMATION;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 50.99
Matches 89; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Duprat, Fabrice APPLICANT: Lesage, Florian
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OTHER INFORMATION: TASK
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                                                                                                                                                 131 ATTAT 135
                                                                                      127 TTCAT 131
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US-09-489-039A-106
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7 GCCCCGCACTGGTGGGACCAGCTGCAGGTAGCTCGGAGGTGGACTGGTGCGAGGAC

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US-09-475-515-65
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| Sequence 67, Application US/09475515A
| Patent No. 6602705
| GENERAL INFORMATION:
| APPLICANT: BARRETT, Susan
| APPLICANT: SRIVASTAVA, Indresh
| APPLICANT: LIU, Hong
| APPLICANT: LIU, Hong
| APPLICANT: HARPOG, Karin
| APPLICANT: HARPOG, Karin
| APPLICANT: HARPOG, Karin
| APPLICANT: HARPOG, Karin
| APPLICANT: HARPOG, LALEN CALLER PARTICLES
| APPLICANT: WALKER, Christopher
| APPLICANT: WALKER, Christopher
| TITLE OF INVENTION: INPROVED EXPRESSION OF HIV POLYPEPTIDES AND PRODUCTION
| TITLE OF INVENTION: UNMER: US/09/475,515A
| CURRENT PAPLICANTON UNMER: US/09/475,515A
| UNMER OF SEQ ID NOS: 90
| SOFTWARET PLING DATE: 1999-12-30
| SOFTWARET PRINCE: PATENTIN VET. 2.0
| SEG IN NO. 67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     546 CCTCTGGTGGACCCTGGCCCTGTTCTGCTGGATCAGTGACCGAGCTTTCTGCGAGCTGCT 605
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4.3%; Score 35.4; DB 4; Length 2340;
Best Local Similarity 57.8%; Pred. No. 1.6;
Matches 63; Conservative 0; Mismatches 46; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match

4.3%; Score 35.8; DB 4; Length 1020;
Best Local Similarity 50.3%; Pred. No. 0.77;
Matches 88; Conservative 0; Mismatches 87; Indels 0
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US-09-475-515-67
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 106
LENGTH: 1020
                                                                                                                                                                                                                                                                         ; TYPE: DNA
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-106
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SEQ ID NO 67
LENGTH: 2340
TYPE: DNA
ORGANISM: Artificial Sequence
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; Sequence 68, Application US/09475515A; Patent No. 6602705

US-09-475-515-68

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APPLICANT: BARNETT, Susan
APPLICANT: STR MEGEDE, Jan
APPLICANT: STRVASTAVA, Indresh
APPLICANT: STRVASTAVA, Indresh
APPLICANT: LIAN, Ying
APPLICANT: LIAN, Thorg
APPLICANT: Gratherine
APPLICANT: Greek, Catherine
APPLICANT: Greek, Catherine
APPLICANT: Greek, Catherine
APPLICANT: Mark
APPLICANT: Mark
APPLICANT: Greek, Catherine
APPLICANT: Mark
APPLICANT: OF UNUBLES, CATHER PARTICLES
FILE REFERENCE: 1621.002
FURENT APPLICATION NUMBER: US/09/475,515A
CURRENT FILING DATE: 1999-12-30
NUMBER OF SEQ ID NOS: 90
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 65
APPLICANT: ZUR MEGEDE, Jan
APPLICANT: ZUR MEGEDE, Jan
APPLICANT: SURVASIAVA, Indresh
APPLICANT: LIAN, Ying
APPLICANT: LIAN, Ying
APPLICANT: LIAN, Hong
APPLICANT: LIU, Hong
APPLICANT: BLBY, Mark
APPLICANT: BLBY, Mark
APPLICANT: WALKER, Christopher
APPLICANT: WALKER, Christopher
TITLE OF INVENTION: IMPROVED EXPRESSION OF HIV POLYPEPTIDES AND PRODUCTION
TITLE OF INVENTION: OF VIGS-LIKE PARTICLES
TITLE OF INVENTION: ON VIGS-LIKE PARTICLES
CURRENT FILING DATE: 1999-112-30
NUMBER OF SEQ ID NOS: 90
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 68
LENGTH: 2385
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4.3%; Score 35.4; DB 4; Length 2385;
Best Local Similarity 57.8%; Pred. No. 1.6;
Matches 63; Conservative 0; Mismatches 46; Indels 0.
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4.3%; Score 35.4; DB 4; Length 2538;
Best Local Similarity 57.8%; Pred. No. 1.7;
Matches 63; Conservative 0; Mismatches 46; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: gp160.modUS4del 128-194
US-09-475-515-68
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OTHER INFORMATION: Description of Artificial Sequence:
OTHER INFORMATION: gpl60.modUS4.delV1
US-09-475-515-65
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ORGANISM: Artificial Sequence
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Gaps

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us-10-017-410-3.rni

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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: BARNETY Susan
APPLICANT: STIVASTAVA, Indresh
APPLICANT: LIAM, Ying
APPLICANT: LIAM, Ying
APPLICANT: LIAM, Ying
APPLICANT: LIAM, Wark
APPLICANT: Mark
APPLICANT: WarkER, Catherine
APPLICANT: WarkER, Catherine
APPLICANT: WarkER, Christopher
TITLE OF INVENTION: OF VIRUS-LIKE PARTICLES
TITLE OF INVENTION: OF VIRUS-LIKE PARTICLES
TITLE OF SEQ ID NOS: 90
CURRENT APPLICANTION NUMBER: US/09/475,515A
CURRENT FILING DATE: 1999-12-30
NUMBER OF SEQ ID NOS: 90
SOFTWARE: PATENTIN VOICE: 2.0
SEQ ID NO 75
LENGTH: 4472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2427 GTACTGGTGGAACCTGCTGCAGTACTGGAGCCAGGAGCTGAAGAGCAGCGCCGTGAGCCT 2486
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SEQ ID NO 64
LENGTH: 2634
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: gpl60.modUS4
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                                                                                                                                                                                                                                                                                        4.3%; Score 35.4; DB 4; Length 2634; 57.8%; Pred. No. 1.7; tive 0; Mismatches 46; Indels 0
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4.3%; Score 35.4; DB 4; Length 4472;
Best Local Similarity 57.8%; Pred. No. 2.4;
Matches 63; Conservative 0; Mismatches 46; Indels 0;
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OTHER INFORMATION: gpl60.modUS4.delVI/V2.gag.modSF2
US-09-475-515-75
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Sequence 73, Application US/09475515A

Patent No. 6602705

GENERAL INPORMATION:

APPLICANT: BARNETT, Susan

APPLICANT: ZNR MEGEDE, Jan

APPLICANT: SRIVASTAVA, Indresh

APPLICANT: LIAN, Ying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 75, Application US/09475515A Patent No. 6602705
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                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 57.8
Matches 63; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-475-515-75
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                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:

APPLICANT: BARNETT, Susan

APPLICANT: STAVASTAVA, Indresh

APPLICANT: STAVASTAVA, Indresh

APPLICANT: HARTOG, Karin

APPLICANT: HARTOG, Karin

APPLICANT: HARTOG, Karin

APPLICANT: HIJU, Hong

APPLICANT: GELEY, Mark

APPLICANT: GELEY, Mark

APPLICANT: SELEY, Mark

APPLICANT: SELEY, Mark

APPLICANT: SELEY, Mark

APPLICANT: SELEY, Mark

APPLICANT: SELEY, Mark

APPLICANT: WALKER, Christopher

ITILE OF INVENTION: IMPROVED EXPRESSION OF HIV POLYPEPTIDES AND PRODUCTION

ITILE OF INVENTION: JOS

CURRENT APPLICATION NUMBER: US/09/475,515A

CURRENT FILING DATE: 1999-12-30

NUMBER OF SEQ ID NOS: 90

SOSTWARE PATENTING OF USE OF THE PATENTIAL OF THE PATENTIAL OF THE PATENTIAL OF THE PATENTIAL OF THE PATENTIAL OF THE PATENTIAL OF THE PATENTIAL OF THE PATENTIAL OF THE PATENTIAL OF THE PATENTIAL OF THE PATENTIAL OF THE PATENTIAL OF THE PATENTIAL OF THE PATENTIAL OF THE PATENTIAL OF THE PATENTIAL OF THE PATENTIAL OF THE PATENTIAL OF THE PATENTIAL OF THE PATENTIAL OF THE PATENTIAL OF THE PATENTIAL OF THE PATENTIAL OF THE PATENTIAL OF THE PATENTIAL OF THE PATENTIAL OF THE PATENTIAL OF THE PATENTIAL OF THE PATENTIAL OF THE PATENTIAL OF THE PATENTIAL OF THE PATENTIAL OF THE PATENTIAL OF THE PATENTIAL OF THE PATENTIAL OF THE PATENTIAL OF THE PATENTIAL OF THE PATENTIAL OF THE PATENTIAL OF THE PATENTIAL OF THE PATENTIAL OF THE PATENTIAL OF THE PATENTIAL OF THE PATENTIAL OF THE PATENTIAL OF THE PATENTIAL OF THE PATENTIAL OF THE PATENTIAL OF THE PATENTIAL OF THE PATENTIAL OF THE PATENTIAL OF THE PATENTIAL OF THE PATENTIAL OF THE PATENTIAL OF THE PATENTIAL OF THE PATENTIAL OF THE PATENTIAL OF THE PATENTIAL OF THE PATENTIAL OF THE PATENTIAL OF THE PATENTIAL OF THE PATENTIAL OF THE PATENTIAL OF THE PATENTIAL OF THE PATENTIAL OF THE PATENTIAL OF THE PATENTIAL OF THE PATENTIAL OF THE PATENTIAL OF THE PATENTIAL OF THE PATENTIAL OF THE PATENTIAL OF THE PATENTIAL OF THE PATENTIAL OF THE PATENTIAL OF THE PATENTIAL OF THE PATENTIAL OF THE PATENTIAL OF THE PATENTIAL OF THE PATENTIAL OF THE PATENTIAL OF THE PATENTIAL OF THE P
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GENERAL INFORMATION:
APPLICANT: BARNETT, Susan
APPLICANT: STUVASTAVA, Indresh
APPLICANT: STUVASTAVA, Indresh
APPLICANT: LIAM, Ying
APPLICANT: LIAM, WAIG
APPLICANT: LIAM, WAIG
APPLICANT: BEEN, Catherine
APPLICANT: SELBY, Mark
APPLICANT: SELBY, Mark
APPLICANT: WALKER, Christopher
ITLE OF INVENTION: INFROVED EXPRESSION OF HIV POLYPEPTIDES AND PRODUCTION
ITLE OF INVENTION: INFRAVED
GURRENT APPLICANTION UNBER: US/09/475,515A
CURRENT PILING DATE: 1999-12-30
NUMBER OF SEQ ID NOS: 90
SOFTWARE: PATENTIN VEY: 2.0
                                               2346 GTACTGGTGGAACCTGCTGCAGTACTGGAGCCAGGAGCTGAAGAGCAGCGCCGTGAGCTT 2405
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   GCACTGGTGGGACCAGCTGCAGGCTGGTAGCTCGGAGGTGGACTGGTGCGAGGACAACTA 71
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                                                                                                                                                                                                 2391 GTTCAACGCCACCGCCATCGCCGTGCCCGAGGGCACCGCATCATC 2439
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                                                                                                                                                                                                                                                                                                                                                                               Sequence 66, Application US/09475515A
Patent No. 6602705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 12
US-09-475-515-64
Sequence 64, Application US/09475515A
; Patent No. 6602705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA ORGANISM: Artificial Sequence
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                      US-09-475-515-66
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Job time : 75.8343 secs
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APPLICANT: HARTOG, Karin
APPLICANT: LIU, Hong
APPLICANT: Oatherine
APPLICANT: SELBY, Mark
APPLICANT: SELBY, Mark
APPLICANT: MALKER, Christopher
TITLE OF INVENTION: IMPROVED EXPRESSION OF HIV POLYPEPTIDES AND PRODUCTION
TITLE OF INVENTION: OF VIRUS-LIKE PARTICLES
FILE REFERENCE: 1621.002
CURRENT APPLICATION NUMBER: US/09/475,515A
CURRENT FILING DATE: 1999-12-30
NUMBER OF SEQ ID NOS: 90
SOFTWARE: PATENTIN Ver. 2.0
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4.3%; Score 35.4; DB 4; Length 4766;
Best Local Similarity 57.8%; Pred. No. 2.4;
Matches 63; Conservative 0; Mismatches 46; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ) OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: gp160.modUS4.gag.modSF2
US-09-475-515-73
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COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 "Diskette, 1.44 Mb storage
COMPUTER: PRAFES

COMPUTER: PRAFES

SOFTWARE: FASTER

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/485,588

FILING DATE: 7 June, 1995

CLASSIFICATION DATA:

PRIOR APPLICATION DATA:

PRIOR APPLICATION DATA:

RICHARD DATA: 10104ing application

PRIOR APPLICATION DATA: 10214ing application

PRIOR APPLICATION DATA: 10394

FILING DATE: 21 October, 1994

APPLICATION NUMBER: PCT/US/94/1217

FILING DATE: 21 October, 1994

APPLICATION NUMBER: U.S. 08/292,827

FILING DATE: 23 August, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1, Application US/08485588
Patent No. 5688938
GENERAL HYCRMATION: BEGNER
APPLICANT: Edward M. Brown
APPLICANT: Steven C. Hebert
APPLICANT: Forrest H. Fuller:
APPLICANT: OF INVENTION: CALCIUM RECEPTOR-ACTIVE
TITLE OF INVENTION: MOLECULES
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Lyon & Lyon
STREET: Firet Interstate World Center
STREET: Suite 4700
STREET: 633 West Fifth Street
                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 633 West Fi
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90071
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LENGTH: 4766
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APPLICATION NUMBER: U.S. 08/141,248
FILING DATE: 22 OCtober, 1993
APPLICATION NUMBER: U.S. 08/009,389
FILING DATE: 23 February, 1993
APPLICATION NUMBER: U.S. 08/017,127
FILING DATE: 12 February, 1993
APPLICATION NUMBER: U.S. 07/934,161
FILING DATE: 21 August, 1992
APPLICATION NUMBER: U.S. 07/834,044
FILING DATE: 11 February, 1992
APPLICATION NUMBER: U.S. 07/834,044
FILING DATE: 23 August, 1991
APPCRNEY/AGENT INFORMATION:
NAME: Heber, Sheldon O.
REGISTRATION NUMBER: 38,179
REGISTRATION NUMBER: 38,179
REGISTRATION NUMBER: 38,179
REGISTRATION INFORMATION:
TELEFAM: (213) 489-1600
TELEFAM: 67-3510
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERICS:
LENGTH: 5775 base pairs
TYPE: nucleic acid
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LOCATION: 515..3769
OTHER INFORMATION:
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November 20, 2004, 20:53:12; Search time 386.775 Seconds (without alignments) 11567.962 Million cell updates/sec
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GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Semience 3 Appli	Segmence 21. Appl	Semience 151 ann		Segment and	. 4	, 4	. 6		Seminary 77895		
ΩI	US-10-017-410-3	US-10-188-832-21	US-10-295-027-151	US-10-182-447-6	US-10-017-410-1	US-09-945-527-48	US-10-182-447-4	US-10-017-161-2429	US-10-292-798-2069	US-10-425-115-77895	US-10-437-963-77989	US-10-425-115-146588
DB	13	16	15	15	13	10	15	15	15	18	17	18
Query Match Length DB	828	4202	4212	822	4175	744	792	35425	35425	3034	1604	637
Query Match	100.0	98.3	98.3	91.9	80.3	42.3	22.1	6.3	6.3	5.1	5.0	5.0
Score	828	813.6	813.6	761	664.8	350.6	183.4	52.2	52.2	42.2	41.8	41
Result No.	н	8	m	4	S	Q	7	80	6	10	c 11	12

Segmence 17. Appl	5	7 6	87	20	Sequence 32295. A	Sequence 77897, A	Sequence 107231.	Sequence 12261, A	Sequence 27071. A		1369.	24309	86. A				้าก			53388	165,	311,	344,	344,	344,	344	344,	344.	344	344,	344,	34
US-10-002-631C-17	0-264-237-	10-182-	US-10-302-172-875	US-10-767-701-20737	US-10-425-114-32295	5-115-	10-42	US-10-767-701-12261	US-10-029-386-27071	US-10-029-386-13371	US-10-292-798-1369	5-2	1-175-523-86	US-09-746-491-55	US-09-939-484-3	US-09-939-483-3				US-10-425-115	US-10	US-10-191	US-10-123-15	US-1		US-10-141	US-10-14	US-10				US-10-141-759-344
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ALIGNMENTS

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Sequence 3, Application US/10017410
Publication No. US20020115094A1
GENERAL INFORMATION:
APPLICANT: Farnham, Peggy J
APPLICANT: Graveel, Carrie R
TITILE OF INVENTION: Polymucleotide Differentially Expressed in Liver Cancer FILE REFERENCE: 960296.97401
CURRENT APPLICATION NUMBER: US/10/017,410
CURRENT FILING DATE: 2001-12-14
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 3
LENGTH: 828
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                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                   ; LOCATION: (1)..(825)
US-10-017-410-3
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SOFTWARE: Patentin Ver.
SEQ ID NO 21
LENGTH: 4202
                                                                        TYPE: DNA ORGANISM: Homo sapiens
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Sequence 21, Application US/10188932

Publication No. US20040076955A1

GENERAL INFORMATION:

APPLICANT: Mack, David H.

APPLICANT: Aziz, Natasha

APPLICANT: Eos Biotechnology, Inc.

TITLE OF INVENTION: Methods of Diagnosis of Bladder Cancer, Compositions

TITLE OF INVENTION: and Methods of Screening for Modulators of Bladder

TITLE OF INVENTION: and Methods of Screening for Modulators of Bladder

TITLE OF INVENTION: Cancer

TITLE OF INVENTION: Cancer

FILE REPREMENT:

FILE REPREMENT:

PRIOR PELING DATE: 2001-01-02

PRIOR APPLICATION NUMBER: US 60/310,099

PRIOR FILING DATE: 2001-00-03

PRIOR FILING DATE: 2001-01-08

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NUMBER OF SEQ ID NOS: 207
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Pred. No. 2e-248;
0; Mismatches 9; Indels
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US-10-295-027-151
Sequence 151, Application US/10295027
Publication No. US20030232350A1
GENERAL INFORMATION:
          Query Match
Best Local Similarity 98.9%;
Matches 819; Conservative
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Length 822;
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96.0%; Pred. No. 5.4e-232;
ive 0; Mismatches 30;
                                                                                                                                                                                                                                                                                                                                                                                               Sequence 6, Application US/1018247

Publication No. US20030185814A1

GENERAL INFORMATION:

APPLICANT: HOFMANN, Kay

TITLE OF INVENTION: CERAMIDASE

FILE REFERENCE: P68055USO

CURRENT APPLICATION NUMBER: US/10/182,447

CURRENT APPLICATION NUMBER: PCT/EP01/00900

PRIOR FILING DATE: 2001-01-27

PRIOR FILING DATE: 2000-01-27

PRIOR FILING DATE: 2000-01-27

PRIOR FILING DATE: 2000-01-27

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SOFTWARE: PATENTIN VOWER: DE 10011392.3
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Matches 792, Conservative
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LENGTH: 822
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Afar, Daniel
Aziz, Natasha
Ginsberg, Wendy M.
Gish, Kurt C.
                                           Glynne, Richard
Hevezi, Peter A.
Mack, David H.
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Best Local Similarity 98.9
Matches 819; Conservative
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                                                                                                                        CTGATGTGTGCTTTGGCCATGTGGTTTCCCAGGAGGTATTTACCAAAGATCTTTCGGAAT 394
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                                   GAGGACAACTACACCATCGTGCCTGCTATCGCCGAGTTCTACAACACGATCAGCAATGTC 120
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Sequence 48, Application US/09945527

Publication No. US20030055588A1

GENERAL INFORMATION:

APPLICANT: Robison, Keith E.

TITLE OF INVENTION: Nucleic Acid and Protein Homologs

TITLE OF INVENTION: Nucleic Acid and Protein Homologs

TITLE OF INVENTION: Nucleic Acid and Protein Homologs

CURRENT APPLICATION NUMBER: US/09/945,527

CURRENT FILING DATE: 2001-08-29

NUMBER OF SEQ ID NOS: 65

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 48

LEASTH. 744
                                                     95 GAGGACAACTACACTATCGTGCCTGCCATTGCCGAGTTCTACAACACACGATCAGCAACGTC
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35 ATGGGCCCCCCCCCCCTGGTGGGACCACCTGCGGCTGGCAGTTCGGAGGTGGATTGGTGC
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CORGANISM: Homo sapiens
US-09-945-527-48
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Publication No. US20020115094A1

GENERAL INFORMATION:

APPLICAMT: Farnham, Peggy J

APPLICAMT: Graveel, Carrie R

TITLE OF INVENTION: Polynucleotide Differentially Expressed in Liver Cancer
FILE REPERENTE: 2005-9.94.04

CURRENT APPLICATION NUMBER: US/10/017,410

CURRENT FILING DATE: 2001-12-14

SUMMER: Patentin Ver. 2.1

SEQ ID NOS: 4

SEQ ID NOS: 4
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     AACAGTGACATCTACTTAATCTGGACTCTTTTGGTTGTAGTGGGAATTGGATCCGTCTAC
                      GACAGGGGTAGGTTCAAGGTGGTCAGTGTCTGTCTGCGGCTTACGACGTGCCTGGCA
                                                                                                                                                                                                                                                   358 GACCAGGIAGGITCAAGGIGGICGICIGICCIGICTGCAGITAIGACGIGCTGGCA
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80.3%; Score 664.8; DB 13; Length 4175;
Best Local Similarity 87.7%; Pred. No. 6.5e-201;
Matches 726; Conservative 0; Mismatches 102; Indels 0;
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) LOCATION: (35)..(859)
US-10-017-410-1
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145 CACCCGTATGCCCCAGAAGCGCTCCCGCTACATTTACGTTGTCTGGGTCCTCTTCATGATC 204
                                                                                                                                                                     265 GAGATCGCCATCCTGTGGCTCCTGGGCAGTGGCTATAGCATATGGATGCCCCCTCTAT 324
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                                                                                  205 ATAGGCCTGTTCTCCATGTATTTCCACATGACGCTCCAGCTTCCTGGGCCAGCTGCTGGAC
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Sequence 2429, Application US/10017161

PUBLICALION NO. US20030143668A1

GENERAL INFORMATION:

APPLICANT: SUWA, MAKIKO

APPLICANT: ASAL', KIYOSHI

APPLICANT: ASAL', KIYOSHI

TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS

FILE REPREBRUCE: 084335/0152

CURRENT APPLICATION NUMBER: US/10/017,161

CURRENT PILING DATE: 2002-12-18

PRIOR APPLICATION NUMBER: UP 2001/246789

PRIOR FILING DATE: 2001-06-18

NUMBER: PATENT NOS: 2430

SOFTWARE: PATENTIN VEV. 2.1
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NAME/KEY: CDS
LOCATION: (21253)..(21367)
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ORGANISM: Homo sapiens
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NAME/KEY: source
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LENGTH: 35425
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             Score 350.6; DB 10; Length 744; Pred. No. 5.8e-101; 0; Mismatches 9; Indels 0:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 22.1%; Score 183.4; DB 15; Length 792; Best Local Similarity 53.3%; Pred. No. 1.5e-47; Matches 410; Conservative 0; Mismatches 356; Indels 3;
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SQUENCE 4, Application US/10182447

Publication No. US20030185814A1

GENERAL INFORMATION:

APPLICANT: HOFMANN, KAY

APPLICANT: RADT, MARCUS

TITLE OF INVENTION: CERAMIDASE

TITLE OF INVENTION: CERAMIDASE

CURRENT APPLICATION NUMBER: US/10/182,447

CURRENT APPLICATION NUMBER: US/10/182,447

FRIOR APPLICATION NUMBER: DE 10003293.1

PRIOR FILING DATE: 2000-01-27

PRIOR FILING DATE: 2000-01-27

PRIOR PILING DATE: 2000-01-27

PRIOR PILING DATE: 2000-01-27

PRIOR PILING DATE: 2000-01-27

PRIOR PILING DATE: 2000-01-27

PRIOR PILING DATE: 2000-01-27

PRIOR PILING DATE: 2000-01-27

PRIOR PILING DATE: 2000-01-27

SOFTWARE: PERCON NUMBER: DE 10011392.3

FRIOR PILING DATE: 2000-03-09

NUMBER OF SEQ ID NOS: 14

SEQ ID NO 4
                 42.3%;
             Query Match
Best Local Similarity 97.5
Matches 356; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-182-447-4
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Sequence 77895, Application US/10425115
Sequence 77895, Application WS/10425115
Publication No. US20040214272A1
Sequence 77895, Application No. US20040214272A1
SEQUENCAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
TITLE OF INVENTION: Plants
TITLE OF INVENTION: Plants
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT APPLICATION NUMBER: 2003-04-28
SEQ ID NOS: 369326
SEQ ID NO 77895
LENGTH: 3034
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6.3%; Score 52.2; DB 15; Length 35425;
Best Local Similarity 61.3%; Pred. No. 7.9e-05;
Matches 84; Conservative 0; Mismatches 53; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 3034;
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Pred. No. 0.036;
0; Mismatches 43;
                                                                                                                                                                                                                        | FEATURE:
| NAME/KEY: CDS
| LOCATION: (35125)..(35225)
| FEATURE:
| NAME/KEY: modified base
| LOCATION: (35270)...(35369)
| COCATION: (35270)...(35369)
| COCATION: (35200)...(35369)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; FEATURE: ". OTHER INFO: Clone ID: MRT4577_171063C.1: US-10-425-115-77895
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Best Local Similarity 61.3%;
Matches 68; Conservative
                                                                                                                                                                                 CDS (26868)..(27016)
                                                               (23918)..(24055)
                                                                                                             CDS (26460)..(26597)
LOCATION: (21462)..(21603)
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ORGANISM: Zea mays
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LOCATION:
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NAME/KEY:
                                         NAME/KEY:
LOCATION:
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Publication No. U520030235833A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: ASMA, WITAGA

APPLICANT: ABURATANI, HIROYUKI
TITLE OF INVENTION: GUANOSINE TRIPHOSPHATE-BINDING PROTEIN COUPLED RECEPTORS
FILE REPERENCE: 084335/166
CURRENT APPLICATION NUMBER: US/10/292,798
CURRENT APPLICATION NUMBER: 10/017,161
PRIOR FILING DATE: 2001-11-13
PRIOR FILING DATE: 2001-12-18
PRIOR FILING DATE: 2001-06-18
NUMBER OF SEQ ID NOS: 2070
SOFTWARE: PATENTIN VET: 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 35425;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 6.3%; Score 52.2; DB 15; Length Best Local Similarity 61.3%; Pred. No. 7.9e-05; Matches 84; Conservative 0; Mismatches 53; Indels
                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: modified base
LOCATION: (35270) ...(35425)
OTHER INFORMATION: a, t, c, g, unknown or other
US-10-017-161-2429
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                                                          FEATURE:
NAME/KEY: CDS
LOCATION: (23918)...(24055)
FEATURE:
NAME/KEY: CDS
LOCATION: (26460)...(26597)
FEATURE:
NAME/KEY: CDS
LOCATION: (26868)...(27016)
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LOCATION: (21253)..(21367)
FEATURE:
                     CDS
(21462)..(21603)
                                                                                                                                                                                                                                                                                              NAME/KEY: CDS
LOCATION: (35125)..(35225)
FEATURE:
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US-10-292-798-2069
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FEATURE:
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527 AGCIGGGCCICITCICGGGCCICIGGIGGACCCIGGCCCIGITCIGCIGGAICAGIGACC 586
                                                                                                 88 Aggedgedgedgedgedgedreggedgedgedgedgedgedgedgedgedgedged 147
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      67 AACTACACCATCGTGCCTGCTATCGCCGAGTTCTACAACACGATCAGCAATGTCTTATTT 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        162 AACTACTCCGTGACCTGGTACATCGCCGAGTTCTGGAATACAGTGAGTAACCTGATCATG 103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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0
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                                                                                                                                                                                                                                                                                                                                                                                                         208 gerricia circerca cercea centra a contra cercener de contra con 256
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Graff, Jonathon M.
APPLICANT: Muenster, Matthew
TITLE OF INVENTION: METHODS TO IDENTIFY SIGNAL SEQUENCES
TITLE REFERENCE: A34943 090495.0243
CURRENT APPLICATION NUMBER: US/10/002,631C
CURRENT APPLICATION NUMBER: 06/330
PRIOR RILING DATE: 2001-10-31
PRIOR FILING DATE: 2001-66-21
NUMBER OF SEQ ID NOS: 324
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 17
LENGTH: 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Birse et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PA131P1
CURRENT APPLICATION NUMBER: US/10/264,237
CURRENT FILING DATE: 2002-10-04
PRIOR APPLICATION NUMBER: PCT/USO1/16450
PRIOR APPLICATION NUMBER: US 60/205,515
PRIOR APPLICATION NUMBER: US 60/205,515
PRIOR PLING DATE: 2000-05-19
PRIOR PLING DATE: 2000-05-19
NUMBER OF SEQ ID NOS: 2287
SOFTWARE: Patentin Ver. 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 13
US-10-002-631C-17/c
US-10-002-631C-17/c
; Sequence 17, Application US/10002631C;
Publication No. US20030157486A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 615, Application US/10264237 Publication No. US20040009491A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 4.9%;
Best Local Similarity 57.6%;
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CORGANISM: Homo sapiens
US-10-002-631C-17
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ORGANISM: Homo sapiens
FEATURE:
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LENGTH: 636
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                                                                                             APPLICANT: La Rosa, Thomas J.
APPLICANT: La Rosa, Thomas J.
APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Boukharov, Andrey A.
APPLICANT: Boukharov, Andrey A.
APPLICANT: Busharok, Brad
APPLICANT: Li, Ping
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APPLICANT: Kovalic, David K.
APPLICANT: Kovalic, David K.
APPLICANT: APPLICANT: Cao, Yinhua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(53222)8
CURRENT FILING DATE: 2003-04-28
KUMBER OF SEQ ID NOS: 369326
SEQ ID NO 146588
LENGTH: 637
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Pred. No. 0.035;
0; Mismatches 82; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: Clone ID: PAT_MRT4530_77836C.1
US-10-437-963-77989
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US-10-425-115-146588
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OTHER INFORMATION: unsure at all n locations
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Publication No. US20040214272A1
GENERAL INFORMATION:
                   Sequence 77989, Application US/10437963 Publication No. US20040123343A1 GENERAL INFORMATION:
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Best Local Similarity 52.6
Matches 91; Conservative
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ORGANISM: Oryza sativa
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US-10-437-963-77989/c
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NAME/KEY: unsure
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4.9%; Score 40.2; DB 16; Length 636;
Best Local Similarity 57.6%; Pred. No. 0.07;
Matches 72; Conservative 0; Mismatches 53; Indels 0
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4.9%; Score 40.2; DB 15; Length 801;
Best Local Similarity 57.6%; Pred. No. 0.079;
Matches 72; Conservative 0; Mismatches 53; Indels 0.
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Sequence 5, Application US/10182447

Publication No. US20030185814A1

GENERAL INFORMATION:

APPLICANT: HOPMAIN, KAY

APPLICANT: RADT, Marcus

TITLE OF INVENTION: CERAMIDASE

FILE REFERENCE: P68055US0

CURRENT APPLICATION NUMBER: US/10/182,447

CURRENT APPLICATION NUMBER: US/10/182,447

FRIOR APPLICATION NUMBER: DE 1001323.1

PRIOR FILING DATE: 2000-01-27

PRIOR FILING DATE: 2000-01-27

PRIOR FILING DATE: 2000-01-27

PRIOR APPLICATION NUMBER: DE 10011392.3

PRIOR PILING DATE: 2000-03-09

NUMBER OF SEQ ID NOS: 14

SEQ ID NO 5

LENGTH: 801
                                                                                                                                                                                                                                                                                                                        FEATURE:
NAME/KEY: misc feature
CCATION: (631)...(631)
SOTHER INFORMATION: n equals a,t,g, or c
US-10-264-237-615
NAME/KEY: misc feature
LOCATION: (560)..(560)
OTHER INFORMATION: n equals a,t,g, or
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; ORGANISM: Homo sapiens
US-10-182-447-5
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US-10-182-447-5
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99.1%; Pred. No. 2.7e-180;
tive 0; Mismatches 6;
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Best Local Similarity 99.13
Matches 675; Conservative
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TITLE		Todd, Ferri Adams Infer	M.A., iera,S. s,M.D. rring r	Todd, M.A., Tanenbaum, D.M. Ferriera, S., Wang, G., Zhk Adams, M.D. and Cargill, M. Inferring nonneutral evol	aum ',G. rgi	D.M., Civello, D.R., Lu, F., Murphy, Zheng, X.H., White, T.J., Sninsky, I.M. Wolution from human-chimp-mouse	
JOURNAL PUBMED REFERENCE AUTHORS		gene Scien 1467] 2 (h Clark Todd,	gene trios Science 302 14671302 Chases 1 Clark, A.G., Todd, M.A., 7 Ferriera, S.,	gene trios Science 302 (5652), 1960 14671302 2 (bases 1 to 681) Clark,A.G., Glanowski,S. Todd,M.A., Tanenbaum,D.M Ferriera,S., Wang,G., Zh	1), WSk: waum	.1963 (2003) .Nielson,R., Thomas, .Civello,D.R., Lu,I	P., Kejar ., Murphy Sninsky,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia; Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus. 1 (bases to 64).

Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Perriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M. White, T.J., Sninsky, J.J., Inferring nonneutral evolution from human-chimp-mouse orthologous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               148 AIGTGCTIGTITGAIGAGTAIGCAACAIGCITGAACAGIGACAICTACTIAAICTGGACT 207
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus HCM1041 gene, VIRTUAL TRANSCRIPT, partial sequence, AV401891.1 GI:39757877 GSS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA. This sequence was made by sequencing genomic exons and ordering them based on alignment.
                                                                                                                                                                                                                                                                 780 TGCTTCGTACCTGGGCTGTGTGTGTGCTTCCCCTACTTTGATGCTGCCTCAGAGATACCTGA
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Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M.
Direct Submission
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/db_xref="taxon:10090"
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                                                         ENGANCE IN METAZOA; Chordata; Craniata; Vertebrata; Euteleostomi;
ENGANCA MATERIA; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

ELMARNALIA; ENTH-BRIA TO 1022)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-rémail.nih.gov
Tissue Procurement: Dr. David Rowe
CDNA Library Preparation: Invitrogen Corp

CONA Library Preparation: Invitrogen Corp

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bloscience Corporation

Clone distribution: MGC Clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAMA4067 row: j column: 05

High quality sequence stop: 681.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone lib="NHH MGC 134" /clone lib="NHH MGC 134" /note="Vector: pCMV-SPORT6.1; Site 1: EcoRV; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.7 kb. Constructed by ResGen, Invitrogen Corp. Note: this is a NHH MGC Library."
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Pred. No. 5.1e-158;
0; Mismatches 114; Indels 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Mus musculus"
/mol type="mRNA"
/db_xref="kaxon:1000"
/clone="IMAGE:6505924"
/tissue_type="undifferentiated limb"
/lab_host="DH10B (phage-resistant)"
                   Mus musculus (house mouse)
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Best Local Similarity 85.5%;
Matches 708; Conservative C
                                            Mus musculus
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AK085306 HTC 03-APR-2004 Mus musculus 0 day neonate Kidney CDNA, RIKSN full-length enriched library, clone:D630008P07 product:similar to CANCER RELATED GENE-LIVER 1 [Mus musculus], full insert sequence.
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                                                                                                                                             /clone lib="NGI_CGAP_Mam2"
/note="Organ: mammary; Vector: pCMV-SPORT6; Site 1: Sall;
/note="Organ: mammary; Vector: pCMV-SPORT6; Site 1: Sall;
stle_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"
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Matches 561; Conservative 0; Mismatches B1; Indels 0
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                                                                               /tissue_type="timor, biopsy sample"
/dev stage="5 months"
/lab_host="DH108"
                                       /db_xref="taxon:10090"
/clone="IMAGE:6437893"
/mol_type="mRNA"
/strain="FVB/N-3"
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HTC; CAP trapper.
Mus musculus (house mouse)
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1 (bases 1 to 868)
1 Mut-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/Link at:
http://image.llh.gov
Plate: LLAM13955 row: g column: 14
High quality sequence stop: 679.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                     GACAACATGCGTGTGTTTAAGCTGGGCCTCTTCTCGGGGCCTCTGGTGGACCCTGGGCCCTG
                                                                                                                             CCCAGAAGGTATCTACCAAAGATCTTTCGGAATGACAGGGGTAGGTTCAAGGTGGTGGTC
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VERSION KEYWORDS SOURCE ORGANISM

AUTHORS TITLE JOURNAL COMMENT

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Query Match
Best Local Similarity 87.4%;
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                                                                                                                                                                                                                                        Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                               Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,Y., Ishii,Y., Nakamura,S., Hazama,M., Nishiner,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Yojiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yonada,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y. RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer [Genome Res. 10 (11), 1757-1771 (2000)
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Analymis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 1173)
                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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Nature 409, 685-690 (2001)
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URL:http://fantome.gsc.riken.jp/
URL:http://fantom.gsc.riken.jp/.
Location/Qualifiers
                                                                                           Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
weth. Enzymol. 303, 19-44 (1999)
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CALAWWFPRRYLPKIFRNDRGRFKAVVCVLSAITTCLAFIKRAINNISLMILGLPCTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TTCCATGCAACGCTGAGTTTCCTGGGTCAGATGCTTGAAGCTTGCCATTCTGTGGGGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTGATGTGTGTTTTGGCCATGTGTTTTCCCAGGAGGTATTTACCAAGATCTTTCGGAAT
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                                                                                                                                                                                                                   /note="unnamed protein product; putative similar to CANCER RELATED GENE-LIVER 1 [Mus musculus] (SPTR|AAL40408, evidence: FASTY, 100%ID, 77.8%length,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               <u> ATGGGCCCCCCCACTGGTGGGACCAGCTGCAGGCTGGTAGCTCGGAGGTGGACTGGTGC</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTGCTCATCGCAGAGCTAAAGAGGTGTGACAACATGCGTGTGTTTAAGCTGGGCCTCTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTGCTTGTTGCAGAGCTGAAGAGGTGTGAATGTGCGTGTGTTTAAGCTGGGCCTCTTC
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0
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                                                                                                                                     enriched mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 512.4; DB 3;
Pred. No. 8.4e-135;
0; Mismatches 81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     81;
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                                                                           /clone="b630008P07"
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/clone lib="RIKEN full-length
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72. _731
                                                                                                                                                                                                                                                                                                                              /codon_start=1
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/db_xref="G1:26351559"
strain="C57BL/6J"
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RESULT

/organism="Mus musculus"

634

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Rattus.

1 (Dases 1 to 565)

Shultz,M.A., Zhang,L., Gu,Y.-Z., Baker,G.L., Fannuchi,M.V., Padua,A.M., Gurske,W.A., Morin,D., Penn,S.G., Jovanovich,S.B., Plopper,C.G. and Buckpitt,A.R.
Gene expression analysis in response to lung toxicants: I. Sequencing and microarray development
Am. J. Respir. Cell Mol. Biol. 30 (3), 296-310 (2004)
Contact: Shultz MA
Contact: Shultz MA
Dept. of Molecular Biosciences, School of Veterinary Medicine
University of California, Davis
1311 Haring Hall, One Shields Avenue, Davis, CA 95616, USA
Tel: 530 752 4698
Email: mashultz@ucdavis.edu
Average Phred score is 20 or better. All poor quality data (Phred < 20) and vector/linker sequence has been removed.
10cation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CF115220 Shultzomica08471 Rat lung airway and parenchyma cDNA libraries Rattus norvegicus cDNA clone NP6159 S', mRNA sequence. CF115220. GI:33175919
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/dev stage="adult"
/clone lib="Rat lung airway and parenchyma cDNA libraries"
/note="Organ: lung; Vector: pGEM-11Zf(-); Site_1: Eco RI;
Site_2: Not I; mRNA was isolated from microdissected rat
lung airways and parenchyma tissues."
                                                                         395 GACAGGGCAGGTTCAAGGCAGTGGTGTGTGTCTGTCTGCAATTACAACGTGCTTGGCG 454
                                    GACAGGGGTAGGTTCAAGGTGGTGGTCAGTGTCTGTCTGCGGTTACGACGTGCCTGGCA 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 218 TAGTGGGAATTGGATCCGTCTACTTCCATT-TTACCCTTAGTTTCTTGGGTCAGATGCTT 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae;
                                                                                                                                                                                                                               rrrarcaagcccgccarcaacaararrrcccrgargarrcrgggacrrccargcacrgcg
                                                                                                                                                                                                                                                                                                                                                                                                                             TCGGGCCTCTGGTGGACCCTGGCCCTGTTCTGCTGGATCAGTGACCGAG-CTTTCTGCGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCTGCTGT-CATCCTTCAACTTCCCCTACCTG 630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 635 gergerecerectricactricectracere 666
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/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="NP6159"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rattus norvegicus (Norway rat)
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Best Local Similarity 88.8
Matches 502; Conservative
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CF115220
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Robert Strausberg, Ph.D.
Email: Ggapba-r@mail.nih.gov
Tissue Procurement: Dr. Jonathan Kuo, NIMH
CDNA Library Preparation: Michael Brownstein Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Biosocience Corporation
Clone distribution: MCC clone distribution information clone distribution: MCC clone distribution information on thrup://image.lnl.gov
http://image.lnl.gov
Plate: LLCM3088 row: p column: 08
High quality sequence stop: 536.
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                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. I (bases 1 to 797)
MIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                       CA463294 797 bp mRNA linear ES7
AGENCOURT_10691314 NIH_MGC_169 Mus musculus cDNA clone
INAGE:6770649 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   58.0%; Score 480; DB 6; Length 797; 87.0%; Pred. No. 1.3e-125; ive 0; Mismatches 80; Indels
                                                                                                                                                                                                                            Mus musculus (house mouse)
                                                                                                                                                            CA463294.1 GI:24919646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 87.0°
Matches 550; Conservative
                                                                                                                                                                                                                                                          Mus musculus
                                                                                                                                  CA463294
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                                                                                                                                                                                                                  SOURCE
ORGANISM
                                                            DEFINITION
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AUTHORS
TITLE
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Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The following the following the following the following following the following following following following following following following following following following following following following following following following following following following following following following following following following following following following following following following following following following following following following following following following following following following following following following following following following following following following following following following following following following following following following following following following following following following following following following following following following following following following following following following following following following following following following following following following following following following following following following following following following following following following following following following following following following following following following following following following following following following following following following following following following following following following following following following following following following following following following following following following following following following following following following following following following following following following following following following following following following following following following following following following following following following following following following following following following following following following following following following following following following following following following following following following following following following following following following following following following following following following following follow
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            241 TGTGACAACATGCGTGTGTTTAAGCTGGGCCTCTTCTCGGGCCTCTGGTGGACCCTGGCC
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                                                                                            /clone lib="781 (synonym: hlcc4)"
/note="Vector: pSport1_Sfi; Site_1: SfiIA; Site_2:
cDNA-collection"
                                                                                                                                                                                                                                                       Length
                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                    Score 447.4; DB 5;
Pred. No. 2.3e-116;
0; Mismatches 1;
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/clone="DKFZp781B0790"
/dev_stage="adult"
/lab_host="DH108"
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BB660847.1 GI:16494626
                                                                                                                                                                                                                                                       tch 54.0%; al Similarity 99.8%; 448; Conservative
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Best Local S:
Matches 448
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T (bases 1 to 449)
Wambut, R., Heubner, D., Mewes, H.W., Weil, B., Amid, C., Osanger, A., Fobo, G., Ran, and Wiemann, S.

EST (Wambutt, R., Heubner, D., Mewes, H.W., Weil, B., Amid, C., et al.)
Unpublished (2003)
                                                                                                         GATGAACTTGCCATTCTTTGGGTTCTGATGTGTGTCTTTGGCCATGTGGTTTCCCAGGAGG 120
                                                                                                                                                                                                  396
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This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s wiemann@dkfz- heidelberg.de;
sequenced by AGGWA (Berlin/Germany) within the cDNA sequencing
consortium of the German Genome Project.

No sl sequence available.

No sl sequence available.
Phis clone (DKFZp781B0790) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERWANY; Email: clone@rzpd.de.
                                                                                                                                                                                                                                   TCTGCAGTTACAACATGCCTGGCGTTTGTCAAGCCTGCTATCAACAATATCTCTCTGATG
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                                                                        GATGAACTTGCAGTCCTTTGGGTTCTGATGTGTGCTTTGGCCATGTGGTTCCCCCAGAAGG
         TAGTGGGAATCGGATCTGTCTACTTCCAINGCAACTCTTAGTTTCCTGGGTCAGATGCTT
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/mol_type="mRNA"
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BX646596.1 GI:34480929
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RESULT 9 BX646596 LOCUS

ACCESSION VERSION KEYWORDS SOURCE ORGANISM TITLE JOURNAL COMMENT

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USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4396
Emax: 402 762 4390
Email: smithfoemail.marc.usda.gov
Single pass sequencing. Bases called and alt trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.
FOR PRIMERS
FOR PRIMERS
FORMARD: AGGAAACAGCTATGACCAT
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Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle Genome Res. 11 (4), 626-630 (2001)
Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
                                                                                                                                                                                                                                                                                    GACAGGGGTAGGTTCAAGGTGGTCAGTGTCCTGTCTGCGGTTACGACGTGCCTGGCA
                                                                                 TTCCATTTTACCCTTAGTTTCTTGGGTCAGATGCTTGATGAACTTGCAGTCCTTTGGGTT
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/lab_host="DH10B"
/clone_lib="MARC_2BOV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     609 TTTGGCCTTGTGGTGGACTCTGGC 632
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Plate: 96 row: L column: 24
Seg primer: ATTTAGGTGACACTATAG.
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/db_xref="taxon:9913"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara, Y. and Hayashizaki, Y.
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Kondo, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamanaka, I., Aizawa, K., Pukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and
                                       Email: genome-resaggsc.riken.jp, URL:http://genome.gsc.riken.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Matahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T.,
and Hayashizaki,Y.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hayashizaki, Y. Computational Analysis of Full-Length Mouse cDNAs Compared with Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone_lib="RIKEN full-length enriched, 0 day neonate kidney"
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/tissue_type="kidney"
/dev_stage="0 day neonate"
/lab_host="DH10B"
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/db_xref="taxon:10090"
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TTGATGAGTA Gaps

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698 bp mRNA linear EST 26-NOV-2002
CSEQCHN24 Gallus gallus cDNA clone ChEST757k21 5', mRNA
                                                            /product="PP11646"
/product="PP11646"
/protein_id="AAQ15241.1"
/db_xref="G1:33341740"
/db_xref="G1:33341740"
ELAVLWYLMCALAMPRRYLPRYLPRNDRGRPKVVSVLSAVTTCLAFVKPAINNISL
MTLGVPCTALLIAELKRHERNQRRRHRKGGQQGGGDKV"
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Gallus gallus (chicken)
Gallus gallus
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TCCTTGCACTGCACTCCTCGCAGAGCTAAAG----
/organism="Homo sapiens"
            /mol_type="mRNA"
/db_xref="taxon:9606"
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                                                      /codon_start=1
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Zhang, P. P., Zhou, X.M., Jiang, H.Q., Huang, Y., Qin, W.X., Zhao, X.T., Wan, D.F. and Gu, J.R.
Direct Submission
Submitted (16-APR-2001) National Laboratory For Oncogenes & Related Genes, Shanghai Cancer Institute, 25/In 2200 Xie-Tu Road, Shanghai 200032, P. R. China
Location Qualifiers
1. 1527
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Handy,Y., Zhou,X.M., Zhang,P.P., Jiang,H.Q., Qin,W.X., Zhao,X.T.,
Wan,D.F. and Gu,J.R.
Novel human cDNA clones with function of inhibiting cancer cell
                                                                                                                                       61
                                                                                                                                                              9
      /note="Vector: pGMV SPORT6; Site 1: NotI; Site 2: SalI; Library made from pooled tissue from testis, thymus, semitendonosus muscle, longissimus muscle, pancreas, adrenal, and endometrium."
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                                                                                                                                       TGGGCGCCCCGCACTGGTGGGACCAGCTGCTGGTAGCTCGGAGGTGGACTGGTGCT
                                                                                                                1;
                                                                                  50.3%; Score 416.2; DB 4; Length 498; larity 91.1%; Pred. No. 2e-107; Conservative 0; Mismatches 43; Indels 1
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Homo sapiens PP11646 mRNA, complete cds.
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467 537 501 550

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/ Organisms="waltus galtus"
/ wol type="mkny"
/ strain="white Leghorn, Hisex"
/ db type="mkny"
/ clone="ChEST323;2"
/ dev_stage="22"
/ lab_bost="blib"
/ clone lib="CSECHN24"
/ note="Organ: heads; Vector: pBluescript II KS(+); Site_1:
ECORI; Site_2: Not!; This normalized library was
constructed from 1 million independent clones. CDNA
synthesis was initiated using an oligo(dT) primer, using
methylated C in the first strand synthesis reaction.
Following this first strand reaction, double-stranded cDNA
was blunted, ligated to Not! adapters, digested with
ECORI, size-selected, and cloned into the Not! and ECOR!
Compatible sites of a custom modified MCS of the
pBluescript (KS:) vector: The library was normalized in 2
rounds using conditions adapted from Soares et al., PNAS
(1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6
reannealing hybridization was used."
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603409105F1 CSEQCHN24 Gallus gallus cDNA clone ChEST323j2 5', mRNA
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Phasianinae; Gallus.

Boardman, P. E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E., Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J. Curr. Biol. 12 (22), 1965-1969 (2002)
                      361 AAAGCTTTTTGTGAGAICTGGTCATTTAACTICCCCTATTTGCACTGTGTATGGCAC 420
                                                                                                                                                                                                                                                                    ATCCTCATCTGCCTTGCCTACCTGGGCTGTATGCTTTGCCTACTTTGATGCTGCC
                                                                                                706 TCAGAGATTCCTGAGCCAAGGCCCTGTCAAGTTCTGGCCCAATGAGAAATGGGCCTTC
                                                                                                                                                                                             481 TCCGAGATCCCTGAGGCCCCGTCATAAAGTTCTGGCCAAGTGAGAGATGGGCATTC
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University of Manchester Institute of Science and Technology
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Location/Qualifiers
1. .781
/organism="Gallus gallus"
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Tel: 01612008930
Fax: 01612360409
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Gallus gallus
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Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1 (bases I to 690)
Boardman, P. E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E.,
Fong, W. T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.
A Comprehensive Collection of Chicken cDNAs
Curr. Biol. 12 (22), 1965-1969 (2002)
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University of Manchester Institute of Science and Technology
(UMIST)
PO Box 88, Manchester, M60 1QD, UK
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48.7%; Score 403; DB 5; Length 69
Best Local Similarity 79.3%; Pred. No. 1.3e-103;
Matches 478; Conservative 0; Mismatches 125; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Gallus gallus"
/mol_type="mRNA"
/strain="White Leghorn, Hisex"
                                                                                                                                                                                                                                                                                                           Tel: 01612008930
Fax: 01612360409
Email: Simon.Hubbard@umist.ac.uk.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="taxon:9031"
/clone="ChEST757k21"
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                                                                                                                                                                                                       Contact: Simon Hubbard
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Email: cdna@lgsun.grc.nia.nih.gov
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Seg primer: M13 Reverse
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Piao,Y., Ko,N.T., Lim,M.K. and Ko,M.S.H.
Construction of long-transcript enriched cDNA libraries from submigrogram amounts of total RNAs by a universal PCR amplification
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B0812G07-5 NIA Mouse Newborn Kidney CDNA Library (Long 1) Mus musculus cDNA clone NIA:B0812G07 IMAGE:30468654 5', mRNA sequence.
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                                                                                                                   ATTGGATCCGTCTACTTCCAT-TTTACCCTTAGTTTCTTGGGTCAGATGCTTGAAGT
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National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
                                                                      Gaps
                                                                      ..
                       Length 781;
                                                                         Indels
                       Score 381; DB 5; Le
Pred. No. 2.6e-97;
0; Mismatches 125;
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                            46.0%;
                  Query Match
Best Local Similarity 79.0°
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CF169369
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                                                                                                                                                                                                      /dev_stage="Newborn Kidney"
/lab_host="DH10B"
/clone_lib="NIA Mouse Newborn Kidney cDNA Library (Long
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    recartringing received and the controcartring received and received and received and received and received and received and received and received and received and received and received and received and received and received and received and received and received and received and received and received and received and received and received and received and received and received and received and received and received and received and received and received and received and received and received and received and received and received and received and received and received and received and received and received and received and received and received and received and received and received and received and received and received and received and received and received and received and received and received and received and received and received and received and received and received and received and received and received and received and received and received and received and received and received and received and received and received and received and received and received and received and received and received and received and received and received and received and received and received and received and received and received and received and received and received and received and received and received and received and received and received and received and received and received and received and received and received and received and received and received and received and received and received and received and received and received and received and received and received and received and received and received and received and received and received and received and received and received and received and received and received and received and received and received and received and received and received and received and received and received and received and received and received and received and received and received and received and received and received and received and received and received and received and received an
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ligation mixture by the standard chemical method. The average insert size is about 3.0 kb. The library was constructed by Yulan Piao."
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/organism="Mus musculus"
/mol_type="mRNA"
/srrain="C5Pul/6J"
/db_xref="niaEST:80812G07-5"
/db_xref="taxon:10090"
/clone="NIA:B0812G07_IMAGE:30468654"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 372.6; DB 6;
Pred. No. 5.8e-95;
0; Mismatches 69;
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421 AATATTTCCCTGATGATTCTGGGACTTCCATGCACTGCGCTGCTTGTTGCAGAGCTGAAG 480

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Search completed: November 21, 2004, 06:57:34 Job time : 2289.57 sec8